

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number #80133

TO: Ruixiang Li

Location: 4c75 / 4c70

Tuesday, February 28, 2006

Art Unit: 1646

Phone: 571-272-0875

Serial Number: 10 / 618570

From: Jan Delaval

Location: Biotech-Chem Library

Remsen 1a51

Phone: 571-272-2504

jan.delaval@uspto.gov

Search Notes	



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My

STIC-Biotech/ChemLib

180/33

From:

Li, Ruixiang

Sent:

Tuesday, February 21, 2006 4:59 PM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search of Application No.10/618570

Please do a standard search on:

SEQ ID NOS: 1 and 2 against nucleic acid databases (excluding pending databases).

Thank you very much!

Ruixiang Li GAU 1646 REM 4D75 Mail Box 4C70 (571) 272-0875

Searcher:

Searcher Phone:

Date Searcher Picked up:

Date completed:

Dat

Type of Search
NA#_____AA#:____
S/L:____Oligomer:____
Encode/Transl:_____
Structure #:_____Text:___
Inventor:_____ Litigation:____

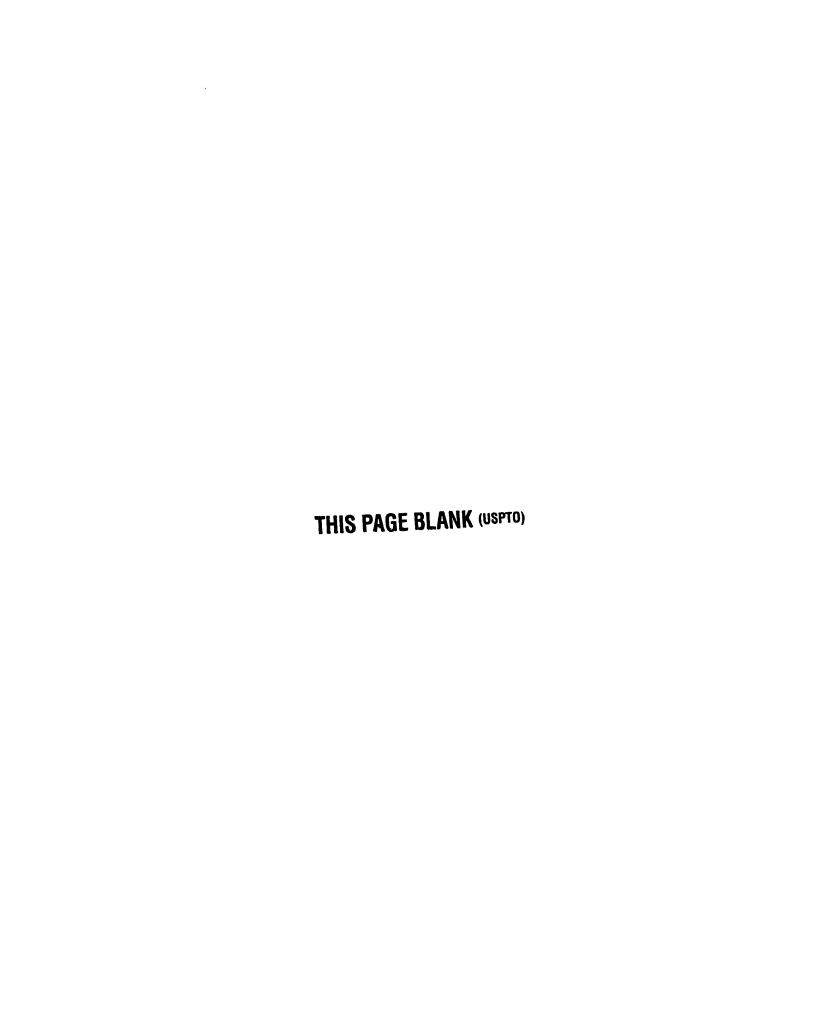
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WWW/Internet:____
Other (Specify):_____

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us-10-618-570-2.ra1

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Patent No. 5510466
Patent No. 5510466
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CK287297 B56 bp mRNA linear EST 02-AUG-2004 EST50019 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMB815 5' end, mRNA sequence.

RESULT 2 CK287297 LOCUS DEFINITION

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/tissue_type="abjoit and biotic stress-treated leaves, tissue_type="abjoit and biotic stress-treated leaves, callus tissue and root tissue"

/lab host="blubl0s-Tonm"
/lab host="blubl0s-Tonm"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
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/note="Vector: pCWNSport6.1; Site 1: ECORI; Site 2: NotI;
/note="Vector: pCMNSport6.1; Site 1: ECORI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (3s C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Feeudomonas syringae pv comato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv campestris 12 hr, and Xanthomonas
campestris pv vesicaticia l8hr). RNA was isolated from
these tissues and pooled in approximately equal molar
                                                                                                     Enkaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; steratophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; steratophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; steratophyta; Magnoliophyta; Solanaceae; Nicotiana.

1. (bases 1 to 856)

2. Stankawicz B., Jin, H. and Baker, B.

3. Generation of EST sequences from Nicotiana benthamiana

3. Unpublished (2003)

3. Other_ESTS: EST750020

3. Other_ESTS: EST750020

3. Other_ESTS: EST750020

3. Other_ESTS: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/.
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Mod Lype="mRNA"
/db xref="t=xon:4100"
/clone="NBMB815"
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
sterids; lamiids; Solanales; Solanaceae; Nicotiana.

El (Bases I to 310)
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other_ESTs: EST75063
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: pocato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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/tissue type="abiotic and biotic callus Tissue and root tissue"
/lab_host="nBl10B-TonA"
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/db_xref="taxon:4100"
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tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (52 3 hr, 6hr), and pathogen challenged leaves (Foeudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; seudomonas syringae pv phaseolicola 18hr; and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar
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                                                                                                                                                                                                                                                                                                                          GATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GGACGAGGCAGCGCCTATCGTGGCTGCCCACGACGGCGTTCCTTGCGCAGCTGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       664 AGCGTTGGCTACCGGTGATATTGCTGAAGAGCTTTGGCGGCGAATGGGCTGACGGTTCCT
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                                                                                                                                                                                                              910;
                                                                                                                                                                                                              Length
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                                                                                                                                                                                                            Score 812.4; DB 7;
Pred. No. 5.3e-211;
0; Mismatches 1;
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                                                                                                                                                                                                            Query Match
Best Local Simil
Matches 813; C
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Solanum tuberosum (potato)
Solanum tuberosum (potato)
Solanum tuberosum
Busaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sparmarophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
sparerida; lamids; Solanales; Solanaceae; Solanum.

I (bases 1 to 936)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTS from potato callus tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA GTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CK256977 936 bp mRNA linear EST 30-JUL-2004 EST740614 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCD170 5' end, mRNA sequence.
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/db_xref="texon:4113"
/clone="POCD170"
/tissue_type="callus"
/lab_host="PHIOB-TonA"
/clone_lib="pocato callus cDNA library, normalized and full-length"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAGTATCCATCATGGCTGATGCAATGCG
                                                           346 TCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCG
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                                                                                                                               GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCAT
                                                                                                                                                         GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCAT
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AUTHORS
TITLE
JOURNAL
COMMENT
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CK256977
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="NRMC477"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab host="DHIOB-TODA"
/clone_lib="NHIOB-TODA"
/clone_lib="NHIOB-TODA"
/clone_lib="NHIOB-TODA"
/clone_lib="NHIOB-TODA"
/clone_lib="NHIOB-TODA"
/lotes="Vector: pCMVSport6.1; Site_l: BCoRI; Site_2: NotI;
/notes="Vector: pCMVSport6.1; Site_lib="Site_2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-estressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae py tomato 12 hr;
Xanthomonas campestris py campestris 12 hr, 18hr;
Pseudomonas syringae py phaseolicola 18hr, and Xanthomonas
campestris py vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
                          CK291799 933 bp mRNA linear EST 02-AUG-2004 EST754513 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMC477 5'
                                                                                                                                                                                                                                                                                                                        E 1 (bases 1 to 933)
Statement, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTS: EST754514
Contact: Robin Bull:
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-arrayetigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGC 3848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 GATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGG 105
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                                                                                                                                                                                                                             Nicotiana benthamiana
Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                  end, mRNA sequence.
CK291799
CK291799.1 GI:39872608
                                                                                                                                                                                                     Nicotiana benthamiana
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VERSION
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GI:39885354

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Spermatophyta, Spermatophyta, Spermatophyta, Spermatophyta, asterids, lamida, Solanales, Solanaceae, Nicotiana.

1 (bases 1 to 947)

1 (bases 1 to 947)

Staskawicz, Harty, Zismann, V., Kazamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
                                                                                                                                                                                                                                                            The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Bmail: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
                                       Nicotiana benthamiana
Nicotiana benthamiana
                                                                                                                                                                                                           Unpublished (2003)
Other_ESTs: EST760923
                                                                                                                                                                                                                                                 Contact: Robin Buell
 CK298208.1
EST.
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/organism="Nicotiana benthamiana" /mol_type="mRNA" /db_xref="taxon:4100"

/clone="MRMDE30"
/tissue type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab host="DH10B-TONA"
/lab host="DH10B-TONA"
/clone lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSport6.1; Site 1: BCORI; Site 2: NoLI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-est-sesed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar 3848 3968 4028 ö 3908 TCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAGTATCCATCATGGCTGATGCAATGCG 4088 GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCAT 4148 136 196 376 256 CGACGITGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGA 316 9/ CTATGACTGGGGCACAACAGACAATCGGCTGCTGATGCCGCCGTGTTCCGGCTGTGTCAGC CTATGACTGGGCACAACAGACAATCGGCTCTGATGCCGCCGTGTTCCGGCTGTGCCAC GATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGG GATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGCGTGGAGGGCCTATTCGG GGACGAGGCAGCGCGCTATCGTGGCTGGCCACGACGGCGTTCCTTGCGCAGCTGTGCT TCTCCCTGTCATCTCACCTTGCTCCTGCTGCAGAAAGTATCCATCATGACTGAGGAAAGGAAAGTATCCATGATGACTGATGCG GGACGAGGCAGCGGCTATCGTGGCTGGCCACGACGACGGCGTTCCTTGCGCAGCGCTGTGCT CGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGA Gaps ö Length 947; Indels Score 812.4; DB 7; Pred. No. 5.3e-211; 0; Mismatches 1; 15.7%; 99.9%; Conservative Query Match Best Local Similarity 4089 257 4029 317 ð 셤 ð 셤

CK298208

EST702-2004

EST760922 Nicotiana benthamiana mixed tissue cDNA library,

normalized, full-length Nicotiana benthamiana cDNA clone NBMDB30 5'
end, mRNA sequence.

CK298208

CK298208 LOCUS DEFINITION

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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 954)
S Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
L Unpublished (2003)
Other ESTS: EST746084
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ATT TAG GTG ACA CTA TAG.
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callus tissue and root tissue."
/lab_host="DH10B-TOA"
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library, normalized, full-length"
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supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCAAGCGAAACATCGCAT 436
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grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (5 C 3 hr, 6hr), and match 2 hr; Astronomes campestris pv campestris 12 hr, 18hr; Setudomonas syringae pv phaseolicola 18hr, and Kanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar 3848 3908 3968 4028 4088 4148 4208 4268 4328 4388 4448 4508 ö 313 373 493 613 673 133 193 253 433 553 733 793 73 TCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCG CGAGGATCTCGTCGTCGTCACCCATGCCGATGCCTGCCGAATATCATGGTGGAAAATGG CCGCTTTTCTGGATTCATCGACTGTGCCGGCTGGGTGTGCCGGACCGCTATCAGGACAT CGTGCTTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGA CGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGA GATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGGCTATTCGG GATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCCCCTTGGGTGGAGAGGCTATTCGG CTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGC craridacrididecadadadaarcegerecrieridaridecegeeererreegerereade CGACGTTGTCACTGAAGGGGAAGGGACTGGCTGCTATTGGGGCGAAGTGCCGGGGGAGGA TCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCGATGCG GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCAT GCATCAGGGGCTCGCGCCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGG gcarcagodorosococoagodoaacriorrosocaagoroaagodogocarocogo GGACGAGGCAGCGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCT CGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGA GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCCAAGCGAAACATCGCAT CGAGCGAGCACCTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGA CGAGGATCTCGTCGTGACCCATGCCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGG CCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGTGGCGGGACCGCTATCAGGACAT AGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTTGGCGGCGAATGGGCTGACCGCTTCCT Gарв CGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGA ; Length 954; IndelB Score 812.4; DB 7; Pred. No. 5.3e-211; 0; Mismatches 1;

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/tissue types.abjoict and biotic stress-treated leaves, /tissue types.abjoict and biotic stress-treated leaves, callus Tissue and root tissue."
/lab_host="blu016-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length."
/note="Vector: pCMVSport6.1; Site 1: ECORI; Site 2: NotI; supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Fecudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris pv campestris pv tomato 12 hr; Pseudomonas syringae pv phaseolicola 18hr; and Xanthomonas campestris and pooled in approximately equal molar
                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamida; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 804)

S Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskandz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)

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Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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CK291519
804 bp mRNA linear EST 02-AUG-2004
EST754233 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMC276 5'
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/organism="Nicotiana benthamiana"
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/db_xref="taxon:4100"
/clone="NBMC276"
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Matches 803;
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BST750907 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMBE61 5'
end, mRNA sequence.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; MagDalantae; Streptophyta; Embryophyta; Core eudicotyledons;
Spermatophyta; MagDalantae; Solanaceae; Nicotiana.

1 (bases 1 to 81)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Generation of EST sequences from Nicotiana benthamiana
302 TCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAGTATCCATCATGGCTGATGCAATGCG 361
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Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualiflers
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                                          GCGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCAT
                                                                            362 GCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCAT
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/lab_host="DHIOB-TonA"
/clone lib="Nktotiana benthamiana mixed tissue cDNA library, normalized, full-length"
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/db_xref="taxon:4100"
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Matches 793; Conservative
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Bos taurus
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/note="Vector: pCMVSport6.1; Site 1: EcoRI; Site_2: NotI; supplier: RNA was isolated from Micotiana benchamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen cold-stressed leaves (5 C 3 hr, 6hr), and pathogen Kanthomonas campestris py campestris 12 hr, 18hr; Pseudomonas syringae py phaseolicola 18hr, and Xanthomonas campestris py vesicatoria 18hr). RNA was isolated from amounts."
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                                                                                                                                                                                                                                                                                                            GCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGAT 3825
                                                                                                                                                                                                                                                                                                                                                                      GGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTA 4005
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                                                                                                                                                                                            Length 811;
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                                                                                                                                                                                           Score 794; DB 7; 1
Pred. No. 5.8e-206;
0; Mismatches 5;
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Best Local Similarity 99.4%;
Matches 797; Conservative (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 793)

S mith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G.,

Wray, J.B. and Keele, J.W.

A second set of bovine ESTS from pooled-tissue normalized libraries

Unpublished (2003)

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4366

Fax: 402 762 4366

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and

trimmed with the aid of the trim_alt option. Vector identified with

cross match v0.999329.

Plate: OQP8005 row: C column: 19

Seq primer: GTAATACGACTAATAGGG.
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              EST 11-MAR-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pooled"
/lab host="DH10B"
/clone_lb="MARC 7BOV"
/note="vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
Library made with RNA pooled from multiple tIssues
including ovary, hindbrain, uterus, and day-30 whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAATCGGTGCTGCCGTCTTTAGGACATATGAAGTATGGCACAGTGGGATGACTTTCCTG
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אפאנו mRNA linear i 1407127 MARC 7BOV Bos taurus CDNA 5', mRNA sequence.
DN548862
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100.0%; Pred. No. 1.1e-205;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                DN548862.1 GI:61013550
EST.
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CF409555 949 bp mRNA linear EST 02-SEP-2003 CH3#061_D06MF Canine heart normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH3#061_D06 5', mRNA sequence.
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Canis familiaris
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                          GTCAGCGCAGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGA
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                                                                                                      3783 ATTCGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCT
                                                                                                                           ATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTCGATGCCGCCTGTTCCGGCT
                                                                                                                                                                                                                                            3903 ACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGCGTTCCTTGCGCAGC
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                                   Score 737.4; DB 8;
Pred. No. 2e-190;
                                                                     .0; Mismatches
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99.9%;
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                                                                       Conservative
                                   Query Match
Best Local Similarity
Matches 738; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Salmo salar"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:8030"
/clone="SNW3-0153"
/cell_type="enriched macrophages"
/dev_stage="adult"
/clone_lib="Atlantic Salmon macrophage - Aeromonas in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           икь96294 767 bp mRNA linear BST 13-JUL-2005
SMV3-0053 Atlantic Salmon macrophage - Aeromonas in vivo infection
DR696294
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                                                                                                    TGCAGTTCAGTATTGAAACACTGAATGGCAGAGTCCAAGAGAATGCATTTAAACAACAAG 1695
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1 (bases 1 to 767)
Douglas, S.E., Tsoi, S.C.M., Penny, S., Melville, K., Liebscher, R. and
                                                                                                                                                                                                                                                                                                                                                                                                      721 ATGAAAAACAAGTATATTTGGAACAGGAAATAAAAGGGGAAATGAAACTGTTGAATAATA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pT-Adv; Libraries (SMV2, SMV3, SMV6, SMV7) made by forward and reverse suppression subtractive hybridization using salmon macrophage infected in vitro for 0.5h (SMV2 and SMV3) or 2h (SMV6 and SMV7) with Aeromonas salmonicida cultured in the intraperitoneal space of fish vs. uninfected macrophages
                                                                                                                      AAAGATTTAATGATGTTCTTTTCCAGCTAAATTCCTTACTTTCCTCCCACCAGGAACATG
                                                                                                                                                                                                                                                            TTCGAGAAGCTGTGATGGAACGCATGAGCAACATGGAAAGCAGAATCCAGTATCTTTCAG
                                                       AGAATATCATAGGGGATATCTCCAAGTCATTAGTAGGTCTGAACACCACAGTACTTGATT
                                                                                                                                                                                               541 AGAATATCATAGGGGATATCTTCCAAGTCATTAGTAGGTCTCAAACACCCACAGTACTTGATT
                                                                                                                                                                                                                                                                                                            AGGAGATGCGTAAATTAGAGGAGCGTATATACAATGCATCAGCAGAAATTAAGTCTCTAG
                                                                                                                                                                                                                                                                                                                                                661 AGGAGATGCGTAAATTAGAGGAGCGTATATACAATGCATCAGCAGAAATTAAGTCTCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Douglas S
Genome Sciences
NRC Institute for Marine Biosciences
1411 Oxford St., Halifax, Nova Scotia B3H3Z1 Canada
Tel: (902) 426-4991
Fax: (902) 426-4913
Email: susan.douglas@nrc.ca
Seq primer: M13R.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ewart, K.V.
Unpublished (2005), Douglas, S.E., et al
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmo salar (Atlantic salmon)
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Contact: Ruley HB
Department of Microbiology and Immunology
Vanderbilt University
Department of Microbiology and Immunology
Vanderbilt University
Department of Microbiology and Immunology
AA4211b, 1161 218t Avenue South, Nashville, TN 37232, USA
Tel: 615 343 7392
Email: ruley@email.mc.vanderbilt.edu
Email: ruley@email.mc.vanderbilt.edu
Sequence tag generated by 3'RACE corresponds to a gene disrupted in mouse BS cells that may be transmitted into the mouse germilne. The inserted entrapment vector can be engineered by Cre-mediated cassette exchange. The 3' end of a split puromycin resistance gene carried by the vector may also be used to select for Cre-mediated chromosome deletion and recombination events. ES cells containing the insertion mutation are available on request.
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                                                                                  1635
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                                                                                                                                                                                                                      1636 TGCAGTTCAGTATTGAAACACTGAATGGCAGAGTCCCAAGAGAATGCATTTAAACAACAAG 1695
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Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Guarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 837)
1 Lin,Q., Donahue,S.L., Cao,S., Moore-Jarrett,T., Osipovich,A.B. and Ruley,H.E.
          829
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Unpublished (2005)
                                                                                  770 recagricagraficaaacacreaareccaeacrecaacacaarecarriraaaccacaae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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CZ169992/c
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Expressed sequence tags from Canine heart
L Unpublished (2003)
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
S29 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2660
Fax: 615 936 2660
Fax: 615 936 2660
High quality sequence stert: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .949
/organism="Canis familiaris"
/organism="Canis familiaris"
/db_Lype="maxon.9615"
/clone="CH3#061_D06"
/tissue_type="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"
/clone_lib="Canine heart normalized cDNA Library in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1036 TAAATCGGTGCTGCCGTCTTTAGGACATATGAAGTATGGCACAGTGGGATGACTTTCCTG 1095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inote="Organ: heart; Vector: pBluescript; Site_1: 5' of vector Not1; Site_2: 3' of vector EooR1; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"
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Pred. No. 4.3e-182;
0; Mismatches 3;
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Best Local Similarity 99.6%;
Matches 709; Conservative
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/tissue_type="abiotic and biotic stress-treated leaves, callus tissue and root tissue"
/lab host="bhi08-TonA"
/lab host="Dhi08-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSport6.1; Site 1: BcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (5 C 3 hr, 6hr), and pathogen
cold-stressed leaves (Feeudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campeetris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
Institute via http://genome.arizona.edu/orders/
Seg primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
                                                                            'organism="Nicotiana benthamiana"
                                                                                                 /mol_type="mRNA"
/db_xref="taxon:4100"
                                                                                                                                      clone="NBMBI49"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%;
ilarity 99.8%;
Conservative
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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                                     704 ATGGCGATAGCTAGACTGGGCGG-TTTATGGTCAGCAAGCGATCCGGATTTGCCAGCTGG
                                                                            GGCGCCCTCTGGTAAGGTTGGGAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCC
                                                                                                                 645 GGCGCCCTTCTGGTAAGGTTGGAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCC
                                                                                                                                                         AAGGATCTGATGGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCG
                                                                                                                                                                               585 AAGGATCTGATGGCGCAGGGATCAAGCTCTGATCAAGAGACAGGATGAGGATCGTTTCG
                                                                                                                                                                                                                                                                                                                      CGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC
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/cell_type="enriched macrophages"
/dev_stage="adult"
/clone_lib="Atlantic Salmon macrophage - Aeromonas in vivo
infectIon"
                                      DR696687 SMV7-0178 Atlantic Salmon macrophage - Aeromonas in vivo infection Salmo salar cDNA clone SMV7-0178, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3812 TCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTG 3871
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 591)
Douglas, S.E., Tsoi, S.C.M., Penny, S., Melville, K., Liebscher, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pr-Adv; Libraries (SMV2, SMV3, SMV6, SMV7) made by forward and reverse suppression subtractive hybridization using salmon macrophage infected in vitro for 0.5h (SMV2 and SMV3) or 2h (SMV6 and SMV7) with Aeromonas salmonicida cultured in the intraperitoneal space of fish vs. uninfected macrophages "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGCGTATCGT 120
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                                                                                                                                                                                                                                                                                                                                                                                            Contact: Douglas S
Genome Sciences
NRC Institute for Marine Biosciences
1411 Oxford St., Halifax, Nova Scotia B3H3Z1 Canada
Tel: (902) 426-4991
Fax: (902) 426-9413
                                                                                                                                                                                                                                                                                                                                          Unpublished (2005), Douglas, S.E., et al Unpublished (2005)
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/organism="Salmo salar"
/mol_type="mRNA"
/db xref="taxon:8030"
/clone="SMV7-0178"
                                                                                                                                                                       Salmo salar (Atlantic salmon)
Salmo salar
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1172 AAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCG 4231
                                          AACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGAGGATCTCGTCGTGACCCATG 4291
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                                                                                                   GTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCC 4402
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AA187083 Plasmid P
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AAV05850 APP-REP 7
AA167595 NUCleotid
AA174524 NUCleotid
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AA25213 PGIRN-EH3
AA3665213 PGIRN-EH3
AA366521 NUCleotid
AA17452 NUCleotid
AA21145 Retrovira
AA36208 NUCleotid
AA3674708 NOVel bic
AA374701 NOVel bic

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

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Scavenger receptor class A; ScR; avidin; fusion protein; bovine; BCD; membrane-spanning domain; extracellular domain; biotin-binding activity;
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                          This invention describes a novel protein (A) which comprises a membrane-spanning domain and an extracellular domain (BCD), where the ECD comprises biotin-binding activity. Using the proteins or encoding nucleic acid molecules it is possible to target biotinylated molecules to specific sites in tissues. Molecules targeted in this way may be taken up by the tissues or cells by endocytosis, allowing the molecules to exert their effects within or on the cell. This sequence encodes a bovine scavenger receptor class Alavidin fusion protein which is used in the description of the invention
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                                                                                                                                                                                                                                                                                                                                                                                     TGAATACCAAACAGGATATCTGTGGTAAGCGGTTCCTGCCCCGGCTCAGGGCCCAAGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                             GATGAGACAGCTGAGTGGGCCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGG
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                                                                                                                                                                     Seguence 5177 BP; 1356 A; 1222 C; 1390 G; 1209 T; 0 U; 0 Other;
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                                                                                                                                                                                                 DB
                                                                                                                                                                                              Score 5165.8;
Pred. No. 0;
0; Mismatches
Page 15-21; 23pp; English
                                                                                                                                                                                                99.8%;
99.9%;
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Best Local Similarity 99.9
Matches 5170; Conservative
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RESULT 2

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CATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTG 4200
                                                                                                                                     GACGAAGAGCATCAGGGGCTCGCCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATG 4260
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1081 GCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAA 4140
                                            CATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTG
                                                                                                                                                                                                                            CAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGAC
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Example 1; Page 25-30; 53pp; English.

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Plasmid pLAiN; retrovirus; gene transfer; mammary gland; milk; lactation; epithelial cell; trans-somatic animal; amylase; chicken; neo gene; cyclic; circular; ds.
                                                                                                                                                                                                                                                Production of a trans-somatic mammal for producing value-added milk - by transferring the gene into the secretory cells of the mammary gland using viral derived particles and their packaging cells.
                                                           Plasmid pLAiN used in retroviral particle delivery.
                                                                                                                                                                                                                   Falconer MM;
                                                                                                                                                                                                                   Nguyen TH, Benkel BF,
        BP.
                                                                                                                                                                                                   (MIAC ) CANADA MIN AGRICULTURE
                                                                                                         Moloney murine leukemia virus
                                                                                                                                                                     98CA-02224108.
                                                                                                                                                                                    97CA-02199212.
        AAV81410 standard; DNA; 7699
                                            (first entry)
                                      (revised)
                                                                                                                                                                                                                                WPI; 1999-035710/04.
                                                                                                                                                                      24-FEB-1998;
                                                                                                                                                                                    05-MAR-1997;
                                    17-0CT-2003
26-APR-1999
                                                                                                                                       CA2224108-A.
                                                                                                                                                       05-SEP-1998
                                                                                                                                                                                                                   Gavora JS,
                                                                                                                  gb
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                                                                                                                Gallus sp.
Chimeric.
                       AAV81410;
AAV81410
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This is the nucleotide sequence of pLANN, a plasmid designed to carry the chicken amylase gene (as a marker protein) and various control sequences chicken amylase gene (as a marker protein) and various control sequences for use in retroviral particle delivery to bovine mammary epithelial cells. The plasmid has the amylase gene and a selectable marker neo gene both under control of the long terminal repeat promoter of the Moloney murine leukamid virus. An internal ribosomal entry site (IRES) provides a translation initiation site within the transcript, allowing the downstream gene product to be produced. A method for producing a transcript sommanal for producing an altered composition of milk computes (1) providing a vector containing a DNA sequence encoding a valuable compound; (2) packaging the vector into a cell line to produce a transcript compound; (2) packaging the vector into a cell line to produce a transcript infecting particle; and (4) delivering the solution into the mammary gland to allow incorporation of the DNA into the accretory cells of the mammary gland. The new method is useful for producing milk with valuable compound and for a changed composition, to enhance its properties and/or marketability. The valuable compound is selected from: an antibody, an extent suppressor prociein, a vormone, a milk protein, a hormone receptor, a tumour suppressor protein, a vaccine, erythropoietin (claimed), a protein content suppressor protein, a promone, a milk protein, a hormone receptor of especially is a tissue plasminogen activator which may be extracted or the milk consumed directly as a therapeutic agent. The new method of concentration and yield of the foreign protein particle. The mammary epithelial cells than prior art methods, resulting in the concentration and yield of the foreign protein particle. The milk consument of more genes can be trans-infected. (Updated on 17-OCT-2003 to consume the concentration and yield of the fersas-infected on 17-OCT-2003 to consume the content of the milk of the foreig

Sequence 7699 BP; 1814 A; 2023 C; 2014 G; 1848 T; 0 U; 0 Other;

Db 11	Qy 10	Db 12	97 11		07				Oy 13:			Oy 14	Db 16	Qy 15(Db 16	Qy 15(Qy 16'	Db 18,	Oy 17:	Db 19(Oy 17	Db 19(Qy 18;	Dp 20:	Oy 19:				Cy 20.		
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40.1%; Score 2077.2; DB 2; Length 7699; nilarity 64.3%; Pred. No. 0;	ches 3339; Conservative 0; Mismatches 1814; Indels 38; Gaps 14;	TITIGAAAGCCCACCCGTAGGTGGCAAACTAAGTTAAGTAACGCACTITIGCAAGGCAT	. GGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGAACAAAAAAC	GGAAAAATACATAACTGAGAATAGAAAGTTCAGATCAAGGTCAGGAACAAGG			181 GATGAGACAGCTGAGTGAGGCCAAACAGGATATCTGTGGTGGTAGGAGTTCCTGCCCCGG 240	355 GATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGG 414	. 241 CTCGGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCGGTTTCTAGTGAA 300	415 CTCGGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA 474	301 TCATCAGATGITICCAGGGTGCCCCAAGAACCTGAAAATGACCCTGTACTTTGAAC 360	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	531 TAACCAATCAGTTCTCTCTCTTCTGTTCCCTTCCCCTTCCCGAGCTCAATAAA 529	421 AGAGCCCACAACCCCTCACTCGGCGCCAGTCTTCCGATAGACTGCGTCGCCCGGGTAC 480		481 CCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGGAATCGTGGTCTCGCTGTTCCTTG 540	655 CCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGTGTTCCTGG 714	GGAGGGTCTCCTCTGGGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT	GGAGGSTCTCCTCTGAGTGATTGACTACCCACGACGGGGTCTTTCATTTTGGGGGCTCGT	601 CCGGGAITTIGGAGACCCTIGCCCAGGACCCACCCACCCACCGGGGGGGGGG	CCGGGATIIIGGAGACCCCIGGCCCAGGGGACCCACCCACCACCACCACCACCACCACCA	835 AGCAACTTATCTGTGTCCCCATTGTCTAGTCTATGTTTGATGTTTATGTTTGTCTGCCCG 894	TCTGTACTAGGTAACTAACTCTGTATCTGGGGACCCGTGGTGGAACTGACGAGTT	TCTGTACTAGTTAGCTAACTCTGTATCTGGCGGACCCGTGGTAGCTGAACTGAGTT	ω	CTGAACACCGGGCGGCGCAACCCTGGGAACGTCCCAGGGACTTTGGGGGGCGTTTTTGTGG	CCCGACCTGAGGAGAGAGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT	CCCGACCTGAGGAAGCGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT	901 AGGAGACGAGAACCTAAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTTCGGTTTGGAA 960	1075 AGGAGACGAGAACCIAAAACAGTICCCGCCICCGCTCIGAATITITGCTITCGGTTICGGA 1134	961 CCGAAGCCGCGTCTTGTCTGCTGCAAGCTTGGGCTGCAGGTCGACTCTAGAGGA 1020	1135 ccGAAGCCGCGCGTCTTGTCTGCTGCAGCACCATCGTTCTGTGTTGTCTCTGTGT 1194	
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Survival; neuron; tyrosine hydroxylase; tyrosine 3-monooxygenase; TH; anti-apoptotic; Bcl-XL; neurological disorder; neuroprotective;
                                                                                                                            Bcl-XL expression directing retroviral vector, pFB-bcl-XL-Sn.
                   ADQ80675 standard; DNA; 7436 BP
                                                                                            (first entry)
ADQ80675
ID ADQ8
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AC ADQ8
XX
DT 21-0
XX
DB BC1-
XX
KW Surv
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The invention relates to a novel method for enhancing the survival of neutrons and/or of cells expressing tyrosine hydroxylase [EC 114.16.2 -
Tyrosine 3-monoxygenase] (TH +) I he method comprises contacting a population of cells with Bol-TW or its functional equivalent, where the population of cells with Bol-TW or its functional equivalent, where the population of cells is selected from: neutrons or cells capable of differentiating into neurons; or TH expressing cells or cells capable of differentiating into TH expressing cells. The invention further composition of isolated mammalian cells overexpressing the anti-apoptotic neutron; an implantable cell culture device comprising; a semi-permeable cell culture device comprising a semi-permeable cell culture device comprising the survival of TH + cells in vivo; a retroviral particle being produced based on a lentiviral transfer vector; enhancing the survival of Th voo differentiated dopamines on a retroviral transfer vector; enhancing the survival of the vool of the survival of the vool of the capable of producing an infective vector particle; treatment of a neurological disorder; a fusion protein comprising the expression vector; and producing comprising the expression vector; and producing comprising the expression vector; and producing membrane capable of directing the expression vector; and producing compression signal, an expression of the fusion protein in a membrane confine for the fusion protein and a promoter of the fusion protein in a medicament useful for the treatment of a medicament useful for the preparation of a medicament commence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydroxylase for the treatment of neurodegenerative disorders. This sequence represents an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enhancing the survival of neurons or cells expressing tyrosine hydroxylase (TH) for treating neurodegenerative disorders, comprises contacting neurons or TH expressing cells with Bcl-XL or its functional
nootropic, antiparkinsonian; transplantation; drug screening;
gene profiling; CNS disorder; neurodegenerative disease; pFB-bcl-XL-Sn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents an expression construct for directing the exp
of Bcl-XL in transduced cells, used in the method for increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        survival rate of neurons of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 6; 108pp; English.
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                                                                                                                                                                                                                                                                                                11-APR-2003; 2003DK-00000581.
22-APR-2003; 2003US-0464546P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-544027/52.
                                                                                                                                                                                                                                                                                                                                                                   (NSGE-) NSGENE AS
                                                                                                                                      WO2004062554-A2
                                                                                         Unidentified.
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Sequence 7436 BP; 1744 A; 1993 C; 1939 G; 1760 T; 0 U; 0 Other;

38.1%; Score 1972.6; DB 13; Length 7436;

GACAGCTGTACAGAGTCTGTGAAGTTCG 1140 GTTACC-----ACTCCCTTAAGTTTG 1081 CATCCTAAAATGGCCCAACTCTTCAAG 1200 cecrcacaaccaercestasarercaas 1141 ACCCTTTATCTCATTGTGTTTGTAGTTC 1260 sargeccarcrrraccrcgargec 1200 CTCCTGAAATGGGAAACGAAGAATTGCA 1320 cccagerradarcaaetrrrrcace 1260 AGTCCGGAAGGCAAAGGAAATGGCAGTG 1380 Acarcereacer---eegaagecerrege 1317 GAACGCATGAGCAACATGGAAAGCAGAA 1440 TACACCCTAAGCCTCCGCCTCCTTCC 1377 CTAGATGCTAAGAATTTCCAAAATTTCA 1500 credriceacceeceriearcricer 1437 CTTTTCCAGCTAAATTCCTTACTTTCCT 1560 GAATTCGATGTACGGGCCAGATATACGC 1497 ACACTGAATGGCAGAGTCCAAGAGAATG 1680 Acegraharesceeceresces 1617 GAGGAGCGTATATACAATGCATCAGCAG 1740 acctarctccaragraacccarade 1677 TTGGAACAGGAAATAAAGGGGAAATGA 1800 virgicercardiceraardeces 1797 AAGTGCTCGCTGACTGGGAAATGGACCA 1920 GTGAACAGCAGAGGTGAATTCACAGGCA 1980 GAGATCAAAGAGTCACCACTGCATGGGA 2040 ACCTITGGCTICACCGICAATIGGAAGT 2100 TGCTTCATAGACAGGAATGGGAAGGAGG 2160 GITCTGTGTTGTCTCTGTCTGACTGTGT 1028 ATCTCCAAGTCATTAGTAGGTCTGAACA 1620 raarcaarracgggggggraragracara 1557 rracegraacrecceacrecederac 1737 CTGAAGGATTGGGAACATTCTCAGACAT 1860 TGGGACTTTCCTACTTGGCAGTACATCT 1854 -----ATGCGGTTTTGGCAGTAC 1901 GGGATTTCCAAGTCTCCACCCCATTGAC 1961 rgrrrregcaccaaaarcaaceegacrr 2002 ricacccharacccccraccccraracc 2059

GGAAGGCAACAGACGGGTCTGACATGGATTGGACGAACCACTGAATTCCGCATTGCAGAG CCCAGCAGCAGA	3210 AGTCAGCAACCCTAACTCCGCCCCTAACTCCGCCCCTAACTCCGCCCCAGTT 3269 3539 GGCTTACATGGCGATAGCTGGCGGTTTTATGGACGAGCGAACTGGATGCTGGATGCTAACTGGAAGTTGCCGGCCCCATGGTTGGCGAGTGCTTTTTTTT	ATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGA	3897 GAATGAACTGCAGGCAGCGCGCCTATCGTGGCTGGCCACGACGGCGTTCCTTG 3956 3624 GAATGAACTGCAGGACGCGCGCCTATCGTGGCTGGCCACGACGGCGTTCCTTG 3956 3624 GAATGACTGCAGGAGGAGGCGGCGCTATCGTGGCCACGACGGCGTTCCTTG 3683 3957 GGCAGCTGTGCTGTGCACTGAAGCGGGAAGGACTGCTGCTATTGGCCGAAGT 4016 3684 CGCAGCTGTGCTGTTGTCACTGAAGCGGCAAGGACTGCTATTGGCCGAAGT 4016 4017 GCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCGCGAGAAAGTATCCATCATGGC 4076 4017 GCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCAGAAAGTATCCATCATGGC 4076 3744 GCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGC 3803 4077 TGATGCAATGCGGCGGCTGCATTCTCACCCTTGCTCCCCATTCGACCACCACCAAGC 4136	3804 TGATGCAATGCGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAGGC 3863 4137 GAAACATCGCATCGAGCGAGCACTCGATGGAAGC 3196 11864 GAAACATCGCATCGAGCGACACGTACTCGATCGATCTGATCAGATGA 4196 11864 GAAACATCGCATCGAGCGACACGTACTCGATCGATCTTGTCGATCAGGATGA 3923 4197 TCTGGACGAAGCGACACGTACTCGAACGCGAACTTTGTCGATCAGGATGA 3923 4197 TCTGGACGAAGAGCATCAGGGCTCGCGCCAGCCTCTTGCCCAGGCTCAAGGCGC 4256 11864 GAACATCGAAGAGATCAGGGCTCGCGCCAACTTTGGCCAGGTCAAGGCGC 3983 4257 CTGGACGAAGAGATCTCGTCGTGCCCAACTGTTGGCGACTCAAGGCGC 3983 4257 CTGGACGAGGGAATCTCGTCGTGACCCAATGGCGATTGCCGAATATCAT 4043 1984 CATGCCCGACGGCGAGGATTCATCGGACTGTGGCGGTTGCCGAATATCAT 4043
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GENE THERAPY RES INST.

99WO-US000733 98US-0071409P

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Expression system containing therapeutic gene and an immunosuppressor gene useful for treating an MHC-I autoimmune disease or killing tumor
                                                                                                                                                                                                                                                            Disclosure; Page 147-151; 154pp; English.
                                                                                                                                                            Radosevich TJ, Link CJ;
                                                                                                                                                                                    WPI; 1999-468988/39.
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                introduction of a therapeutic gene comprising: (1) a nucleotide sequence encoding an immune suppression gene; (11) a promoter; and (111) a transcription termination signal, where the system is able to inhibit, evade or aliminate a recipient cell immune response to the therapeutic gene when the gene is transformed into a recipient cell. AXX90481 to AXX90484 represent specifically claimed plasmid retroviral vector nucleotide sequences from the present invention. The expression system and vectors containing it can be used for gene therapy, for treating an WHC I autoimmune disease or for Killing tumour cells. The expression system contains an immunosuppressive gene which prevents host rejection of the vector. The present sequence represents a plasmid retroviral
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present invention describes a nucleotide expression system for the
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.0%; Score 1916.6; DB 2; Length 7546; Best Local Similarity 64.2%; Pred. No. 0; Matches 3348; Conservative 0; Mismatches 1624; Indels 247; Gaps
                                                                                                                                                                                                                                                                                                                                                                         Sequence 7546 BP; 1695 A; 2066 C; 1981 G; 1804 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                       vector from the present invention, designated pLXSU-IRES-N
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Plasmid retroviral vector; expression system; immunogenic; gene therapy; immune response; immunosuppression; gene delivery; therapeutic; MHC-I autoimmune disease; tumour; ss.

retroviral vector pLXSU-IRES-N nucleotide sequence.

(first entry)

29-SEP-1999

Plasmid

BP.

AAX90485 standard; DNA; 7546

RESULT 4

21;

GGAGATGCGTAAATTAGAGGAGCGTATATACAATGCATCAGCAG 1740 adgeagaadtargeaageargeaterearragreageaacea 1833 TGAAAAACAAGTATATTTGGAACAGGAAATAAAAGGGGAAATGA 1800 Grefercherradgereregaaagreeceagereeceagea 1720 GCAGTTCAGTATTGAAACACTGAATGGCAGAGTCCCAAGAGAATG 1680 rcc--eccercecceraacrececcaerrececcarre 1891 CACTAATGATCTGAGGCTGAAGGATTGGGAACATTCTCAGACAT 1860 chartritritratrandeadaccaaccecececee 1951 ACTCCAAGGTGCCAGAAAGTGCTCGCTGACTGGGAAATGGACCA 1920 ------Trccagaagragragaagacrrrrrrgaagacr 1993 CATGACCATCGGGGCTGTGAACAGCAGAGGTGAATTCACAGGCA 1980 crregecrecaaecrregracceaecreeearceararcreee 2053 AACAGCCACATCAAATGAGATCAAAGAGTCACCACTGCGA 2040 cecrererecearerireesagiaceadirasagrarreesag 2224 GCTGCTGCGGTCAAGTGTTAATGACATTGGTGATGACTGGAAAG 2220 GGTCTAATAGGTACTCCAGGTCTTAAAGGTGATCGGGGGATCT 2400 STICGAGGATICCCAGGACCAATGGGGAAGACCGGGAAGCCAGG 2458 areccaaacriarrareaderecaaccceerecreerec 2510 GTGGGTGGCAGCGCCCTCACGAAGGCAGAGTGGGAGATTTTTCA 2578 accrreraarecrrarreraeccrrreesecccesrceses 2113 CAAGAGGACCCAGCCTTTGGCTTCACCGTCAATTGGAAGT 2100 -----ràrccrrgacrcrrrrcgargaaccrcccccrrggrg 2164 aarcaaacaricaacraaaacarcraraaacccracacaaaac 2284 ACTCCAGGTGAAAAGGAGATAGAGGCCCTCCTGGACAAAATGG 2340 GCCAGAAGGGAGAAAAAGGGAGTGGAAGCATGCAAAGACAATC 2518 sagcregtradaddacaredadeacrarrerreaddarege 2570 ACGGTGTGTGACGACCGCTGGGAACTGCGTGGAGGACTGGTCGT 2638 kereitriresesecreraisraaaserreserecaecaeari 2684 GAATATCATAGGGGATATCTCCAAGTCATTAGTAGGTCTGAACA gacgccccicidadccccccccaaagccccccaaa----TGTCTTCACGGCCAGTGCTTCATAGACAGGAATGGGAAGGAGG

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2639 CTOCHGAGGCTTGGGAATGCAAGGTGTTCAAAGTGGCTCAAGGGGCTCATTTTGGGAAGCCCCCC 274 2699 AGGTGCGAATTATTGCCTGGAATGAAGTGATTTTGGTTGG

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The myoD proximal and distal regulatory regions (See AAQ74447, AAQ74448) may be inserted into vectors such as this and used (1) to induce a muscle phenotype in a non-muscle cell, (2) for positive or negative selection of muscle cells (3) for targetted gene expression, specifically in skeletal muscle, (4) for the expression of genes controlling growth of myoblasts or mutant forms of myoD that modulate muscle differentiation, (5) for changinearing rhabdosarcoma cells to increase sensitivity to chemotherapeutic agents, (6) for the expression of growth factors to stimulate skeletal muscle growth in animals, and (7) to identify nuclear regulatory factors that bind to the regulatory region
                                                                                      Isolated proximal and distal myoD regulatory regions - and vectors contg. them, for tissue selective gene expression in muscle cells and for positive or negative muscle cell selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAAAATACATAACTGAGAATAGGAAAGTTCAGATCAAGGTCAGGAACAAAGAAAAACAGC
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Matches 3536; Conservative
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835 AGCAACTIATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTTGATGTTATGCGCCTGCG 894	721 TCTGTACTAGTTAGCTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTT 780	840	1014 900 1074	AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGAA 960	CCGAAGCCGCGCGTCTTGTCTGCTGCAGCTTGGGCTGCAGGTCGACTCTAGAGGA 1020	TCATTCGGCACGAGTAAATCGGTGCTGCTGTTTAGGACATATGAAGTATGGC 1075	1125	AGTCTGTGAAGTTCGATGCTCGCTCAGTGACAGCTTTGCTTCCTCCCCATCCTAAAAATG 1185	GCCCAACTCTTCAAGAGAGAGAGGATGAAAACTGCACTGATCACCTTTATCTCA 1245	1434		1306 AAACGAAGAATTGCACGTTGGCTCAGTTAATGCAGATATTCTCCAAGTCCGGAAGGCA 1365	AAGGAAATGGCAGTGAAGATG 1386	1555 GGTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCTTTATCCAGCCC 1614 C 1387 AAATGAGATTTCGAGAAGCTGTGATGGAACGCATGAGGAAGCAGCA 1432	TCACTCCTTCTTCTAGGCGCCGGAATTGATCCCGGACCATGAGCTTCAATACCCTGATTGA 1674	1435 ANGLAGAILCAGINITICAGAIANIGAANCCAGINCINGAGAITICCA 1492 1675 CIGGAACAGCIGAACAGCAGCGGGGGGGGGGGGGGGGGG	1493 AAATTTCAGCATAACAACTGATCAAAGATTTAATGATGTTCTTTCCAGCT 1543	AAATTCCTTACTTCCTCCAGGAACATGAGAATATCATAGGG 1589	1854	CACCCCTGAAGAGATGGCGCGCGCGGGGGGGTCTGAGCGAGTTAAAACAGGCGAT 1914	1640 GTTCAGTATTGAAACACTGAATGGCAGATCCAAGAGAATGCATTTAAACAACAAGA 1696 1915 GACCGCTGCCGTCAAAATATTGAAACGTTCCGCGCAGACGCTACCGCCTGTAGA 1974
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ussion system containing therapeutic gene and an immunosuppressor useful for treating an MMC-I autoimmune disease or killing tumor

98US-0071409P

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Claim 25; Page 141-144; 154pp; English.
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therapy; Plasmid retroviral vector; expression system; immunogenic; gene immune response; immunosuppression; gene delivery; therapeutic; MHC-I autoimmune disease; tumour; 88. Plasmid retroviral vector pLXSI-IRES-N nucleotide sequence 뮵 AAX90483 standard; DNA; 7165 (first entry) 29-SEP-1999 Synthetic AAX90483 RESULT 6

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99WO-US000733

13-JAN-1999;

22-JUL-1999

23; 360 120 180 240 420 594 480 540 234 294 414 CTCGGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA 300 474 534 654 714 GGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT 600 The present invention describes a nucleotide expression system for the introduction of a therapeutic gene comprising: (1) a nucleotide sequence encoding an immune supression gene; (ii) a promoter; and (iii) a transcription termination signal, where the system is able to inhibit, evade or eliminate a recipient cell immune response to the therapeutic gene when the gene is transformed into a recipient cell. AAX90481 to AAX90484 represent specifically claimed plasmid retroviral vector nucleotide sequences from the present invention. The expression system and vectors conclaining it can be used for gene therapy, for treating an MHC-I autoimmune disease or for killing tumour cells. The expression system expression an immunosuppressive gene which prevents host rejection 9 GGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGAACAAAGAACAGC TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCTGTACCTTTGAAC 61 GGAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGAACAAGAAACAGC TAACCAATCAGTTCGCTTCTGGCTTCGCGCGCTTCCGCTCTCCGCTCTCCGATAAA ccerarreccaaraaaccrerrecrerrecarceaarcerecrecrecre TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCAT TGAATACCAAACAGGATATCTGTGGTAAGCGGTTCCTGCCCCGGCTCAGGGCCAAGAACA GATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGG GATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGG rcarcagargrirccagggrgccccaaggaccrgaaaargacccrgraccrrarraaac AGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTTCCGATAGACTGCGTCGCCCGGGTAC CTCGGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA TTTGAAAGACCCCACCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCAT TAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCGCTCTCCGAGCTCAATAAA CCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTG Query Match 31.8%; Score 1644.6; DB 2; Length 7165; Best Local Similarity 62.9%; Pred. No. 0; Matches 3284; Conservative 0; Mismatches 1309; Indels 624; Gaps Sequence 7165 BP; 1631 A; 1972 C; 1880 G; 1682 T; 0 U; 0 Other; 175 235 121 295 181 355 241 415 301 475 361 535 595 481 655 541 421 the 셤 용 셤 ò ò 셤 ò 셤 ò ð

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Score 1629.4; Pred. No. 0; 0; Mismatches

31.5%; 98.6%;

Conservative

Similarity

Best Local Sim: Matches 1654;

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Query Match Best Local S

3371 AAGCTTCACGCTGCCGCAAGCACTCCAGGCCGCAAGGCTGCTAAAGGAAGCGGAACACGT

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The invention provides a novel method for directing self-assembly of a gene having three or more fragments in a directionally and spatially ordered fashion to produce a gene or a gene vector. The method involves usage of primers, containing class IIS restriction endomuclease recognition sites, for isolation of these fragments. As described in the disclosure, the method may also use a vector for the incorporation and soreming of endogenous mouse promoter elements for the incorporation and classific promoters. In the example given, plasmids pBK-CW (AAV33626), pVLMB (AAV33623) and pVLOVHGH-900 (AAV33621) were used as templates from which six fragments were amplified. Bach of the fragments contained different regulatory sequences. The six PCR fragments were designed to self-assemble into a retro-vector using the method of the invention. The present sequence, designated as GENSA 981, represents the monomeric DNA sequence of the six ligated fragments. In general, the method is claimed to be useful for isolating and identifying regulatory sequences from a cell, including those for enhanced biological activity, or tissue-specific, hormone-specific or developmental-specific gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembling gene or gene vector - comprises use of primers class IIS restriction endonuclease recognition sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class IIS restriction endonuclease recognition site; endogenous mouse promoter element; tissue-specific gene expression; hormone-specific gene expression; ss;
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Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;

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Unidentified.
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/*tag= b /note= "Retroviral packaging region"

misc_feature

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The invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell. The invention further expression of one or more proteins in a host cell. The invention further provides methods of indirectly detecting the expression of a protein of interest, comprising providing the host cell transfected with a vector desired protein operably linked by an internal ribosome entry site closed protein and the desired protein is produced, where the presence of signal protein and the desired protein is produced, where the presence of signal protein indicates the presence of desired protein. Regulatory elements and vectors of the invention are useful for the expression of proteins of interest in a host cell. They are useful for the expression of chemone, insulin (19), preferably secretory 19; They are useful in the expression of one or more proteins such as erythropoietin, growth commons, von Willebrands factor, into side and their receptors, von Willebrands factor, ind surfactant, serum a blumins, DNase, vascular endothelial growth factors, creeptors for hormones or growth factors, interleaves, or proteins, osteoinductive factors, immunotoxins, proteins, or proteins, osteoinductive factors, interleaves, interleaves, colony stimulating factors, interleavins, and ressins, requirance proteins, and ressins, reduces membrane proteins, and ressins, reduces membrane proteins, or can proteins and their fragments. The vectors and other artibodies, chimeric proteins and their fragments. The vectors and other calls, bovine kidney cells and human kidney cells, including rat finound proteins in elements moloney murine leuvemia virus (Mowlly) 5' LTR, Mowlly viral clements; moloney murine leuvemia virus (Mowlly) 5' LTR, Mowlly INR, phosphotransferase gene and 3' Mowlly INR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel regulatory elements including nucleic acid encoding hybrid alpha-
lactalbumin promoter or mutant RNA export element, for expressing one or
more proteins e.g. antibodies, pharmaceutical proteins in host cells.
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                                                                                                                                        e
"Neomycin phosphotransferase gene"
                      /*tag= c
/note= "Hepatitis B surface antigen"
2279, .2595
/*tag= d
/note= "RSV promoter"
2951. .3745
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66.1%; Pred. No. 0;
cive 0; Mismatches
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4atches 3007; Conservative
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The invention relates to a host cell comprising a genome comprising at least one integrated integrating vector, where the integrated integrating vector where the integrating vector lacks a gene encoding a selectable marker. The invention also relates to a method of transfecting host cells, involving providing a number of host cells comprising a genome and a number of integrating vectors, where the integrating vectors comprise at least one exogenous gene, where the integrating vectors comprise at least one exogenous gene, and where the integrating vectors lack a gene encoding a selectable marker, contacting the host cells comprising at least one integrated copy of the integrating vectors to generate transfected host cells comprising at least one integrated copy of the integrating vector and selecting the transfected host cells. The host cell is useful for producing a protein of interest which involves providing a host cell, where the exogenous gene is stable in the absence of selection. The integrating vector further comprises a secretion signal sequence operably linked to the exogenous gene is table in the absence of selection. The integrating vector further comprises a secretion signal sequence operably linked to protoins for pharmaceuticals and industrial, diagnostic and other purposes, and in the production of multiple variants of proteins.

Considered by analysis of the activity of the protein variants. This sequence represents LSRNL vector DNA, used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Host cell useful for producing proteins for pharmaceuticals, industrial purposes, comprising genome having at least one integrated vector having at least one exogenous gene and lacking selectable marker.
                  CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGGCGCATCGCCTTCT
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Pred. No. 0;
0; Mismatches 754; Indels 786; Gaps
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28-MAR-2002; 2002US-0368357P.
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Best Local Similarity 66.1%;
Matches 3007; Conservative (
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The invention relates to the production of proteins in host cells. The host cells contain multiple integrated copies of an integrating vector comprising an exogenous gene operably linked to a promoter, and where the integrating vector lacks a gene encoding a selectable marker. The invention is used to produce proteins of interest at high levels. The
                                  3600 GCTATCAGGACATAGGGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGGGGGCGAATGGG
                                                                                                            3660 CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCCGATTCGCAGCGCATCGCCTTCT
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/note= "RSV promoter"
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0 961 CCGAAGCCGCGCGTCTTGTCTGCTGCAGCTTGGCTGCAGCTCGAGTCGATCTTAGAGGA	120 Qy 1141 120 Db 1120 0Y 1201	180 Db 1180 240 Db 1240	240 Oy 1321 CGGTTGGCTCAGTTAATGCAGATATATCTCCCAAGTCCGGAAGGCAAAGGAAATGGCAGTG 300 Db 1277 ATATTCCTCTTCATCCTGCTGCTGCTCATCTTGTTGTTGTTGGTCTTCTGGAACCAA 300	360 Db 1337 GGTATGTCCCGTTTCCAGAACTCTCCAGAACCATCAACTACCAAACAGAAA 360 Db 1337 GGTATGTTGCCCGTTTGTCCTCTACTTCCAGGAACATCAACTACCAGAACCAAA 360	A 420 Db 1394 TGCAAGAACTGCTGCTCAGAAGCTATTCCAAGAATTTCCAAAGAATTTCCAAAAGAATTTCTCAAAAATTTCTTCAAAAAATTTCTTCAAAAAAA	480	540 Db 1509 CAAGATTCCTATGGGAGTGGGCCTCAGTTTCTCCTGG	600 1550 -CRAGITITACARIANTICACIANTICACACACICAANAGAATIC	660 Db 1681 CATTTAACAACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	720 Db 1665 CCTTTTTACCTCTATTACCTCTTTTCTTTTGGGTATACATTTAAAAAAAA	780 Db 1725 AAC	840 Qy 1861 TGADADATATCACTTTACTCCAAGGTGCCAGAAGTGCTCGCTGACTGGGAAATGGACCA 1 1 1 1 1 1 1 1 1	T 900 T 1921 ACGATCTGGGCTCCAACATGGGGCTGTGAACAGGAGTGAATTCACAGGGA 1980 Db 1782		AA 960 2041 CACAAAACACCATCAAGAAGACCCAGCCCACCTTTGGCTTCACCGTCAATTGGAAGT 2100
present sequence represents a LSNRL vector. This vector is used to produce proteins in the method of the invention. Sequence 5130 BP; 1187 A; 1335 C; 1332 G; 1276 T; 0 U; 0 Other; Query Match Best Local Similarity 66.1%; Pred. No. 0; Matches 3007; Conservative 0; Mismatches 754; Indels 786; Gaps 1 TTTGAAGACCCCACCCGTAGGTGGCAAGCTAAGTAAGTAA		121 TGAATACCAAACAGGATATCTGGTAAGCGGTTCCTGCCCCGGCTCAGGGCCAAGAACA	181 GATGAGACAGCTGAGTGATGGGCCAAACAGATATCTGTGGTAAGCAGTTCCTGCCCCGG 241 CTGGGGGCCAAAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA	301 TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCTGTACCTTATTTGAAC	361 TAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCGCTCTCCGAGGTCAATAAA 	421 AGAGCCCACAACCCCTCACTCGGCGCCCAGTCTTCCGATAGACTGCGTCGCCCGGGTAC	481 CCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTG	541 GGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGGTCGT	601 CCGGGATTTGGAGACCCCTGCCCAGGGACCACCACCACCACCACCAGGGAAGGTAAGCTGGCC	661 AGCAACTTATCTGTGTCTGTTCGATTGTCTAGTGTCTATGTTTGATGTTATGCGCCTGCG	721 TCTGTACTAGTTAGCTAACTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTT	781 CTGAACACCCGGCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGG 	841 CCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTGTTCTGGT	901 AGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGAA	901 AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAAFTTTTGCTTTCGGTTTGG

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TGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGTGGCGGAGCC 3599
GCATGCCCGACGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCA
                                            TGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGCCGGACC
                                                                                      GCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGG
                                                                                                   GCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCAATGGG
                                                                                                                                   CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCT
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                                                                                                                                                                                         ATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGGTTCGAAA 3766
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/*tag= "R&V promoter"
2951. .3745
/*tag= e
/note= "Neomycin phosphotransferase gene"
4537. .5130
/*tag= f
                                                                                                                                                                                                                                                                                                                          Retroviral vector expressing hepatitis B surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "hepatitis B surface antigen"
                                                                                                                                                                                                                                                                                                                                                cell transduction; transfection;
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*tag= b
'note= "Retroviral packaging region"
                                                                                                                                                                                                                                                                                                                                                gene therapy; cell transduction; production; ds; surface antigen.
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note= "MoMuSV 5' LTR"
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                                                                                                                                                                                                                                                                                                                                                                                Moloney murine sarcoma virus.
Respiratory syncytial virus.
Moloney murine leukemia virus.
                                                                                                                                                                                                                                                         AEB77874 standard; DNA; 5130
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Synthetic.
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                                                                               Transducing host cells useful for producing essential proteins comprises serially contacting host cells with integrating retroviral vectors to provide host cells comprising multiple integrated retroviral vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                  invention relates to transducing host cells comprising providing at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCTTCCGCTCTCCGATCAATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGAAAGACCCCACCGTAGGTGGCAAGCTAAGCTAAGTAACGCCACTTTGCAAGGCAT
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                                                                                                                                                                                                  Example 1; SEQ ID NO 9; 168pp; English
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Best Local Similarity 66.1
Matches 3007; Conservative
                             WPI; 2005-555595/56
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GGAGGGCTCTCCTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT

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	1861 TGAAAATATCACTTTACTCCAAGTGCCAGAAAGGCTCGCTGACTGGGAAATGGACCA	1782TACTTTACCGCAAGACATATTGTACTAAAAATCAAGCAATTTTCG- 2041 CACAAACACCACCCCAGCCCAGCCCACCTTTGGCTTCACCGTCAATTGGAAGT 1830AAAACTGCCTGTAAATAGACCTATTGGAAAGTATGCAAAGGAAGG	1945 GCATGTATACAATCT	2401 CTGGTTTACCTGGAGTTCGAGGATTCCCAGGACCAATGGGGAAGACCGGGACCAGGAC 2040	
CCGGGATTTGGAGACCCCTGCCCAGGGACCACCACCACCGGGAGGTAAGCTGGCC 660	780 840 900 900		1060 AGGACCCCTGCTGCTGATATACTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1240 TCCTGGCTATC 1321 CGGTTGGCTCAGTTAATGCAGATATTCTCCAGGTCGGAAGGAA	1501 GCATAACAACTGATCCAAGATTTAATGATGTTTTTCCAGCTAAATTCCTTACTTTCCT 1560 097 1449

The present invention describes a nucleotide expression system for the introduction of a therapeutic gene comprising: (i) a nucleotide sequence encoding an immune suppression gene; (ii) a promoter; and (iii) a transcription termination signal, where the system is able to inhibit, evade or eliminate a recipient cell immune response to the therapeutic gene when the gene is transformed into a recipient cell. AXSO481 to AAX90484 represent specifically claimed plasmid retroviral vector nucleotide sequences from the present invention. The expression system and vectors containing it can be used for gene therapy, for treating an MHC-I autoimmune disease or for killing tumour cells. The expression system contains an immunosuppressive gene which prevents host rejection of the vector Expression system containing therapeutic gene and an immunosuppressor gene useful for treating an MHC-I autoimmune disease or killing tumor cells. 25; Page 144-147; 154pp; English Claim

Sequence 5874 BP; 1351 A; 1611 C; 1515 G; 1397 T; 0 U; 0 Other;

3751 2090 2210 2270 3991 4051 4171 2510 3811 2150 3871 3931 2330 2390 4111 2450 4231 2570 4291 ö CTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGG AAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAAGCATCAGGGGCTCGCGCCGCCG GATCTGATCAAGAGACAGGATGATCGTTTCGCATGATTGAACAAGATGGATTGCACG 2031 GATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACG CAGGITCICCGGCCGCTTGGGTGGAGGCTATTCGGCTATGACTGGGCACAACAGACAA CAGGTTCTCCGGCCGCTTGGGTGAGAGGCTATTCGGCTATGACTGGGCACAAACAGACAAA reserrecrearsecererrecesersrangesececeeeceeerrarre resectecteratececedestreceserereacecedesecececestrere TCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGCCTTGTTCGT GGCTGGCCACGACGGCGTTCCTTGCGCAGCTGTCGACGTTGTCACTGAAGCGGGAA GGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAA GGGACTGGCTATTGGGCGAAGTGCCGGGCAGGATCTCCTGTCATCTCACCTTGCTC GGGACTGCTATTGGGCGAAGTGCCGGGCAGGATCTCCTGTCATCTCACCTTGCTC CTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGG AAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGGAGCATCAGGGGCTCGCGCCAGCCG AACTGTTCGCCAGGCTCAAGGCGCGCGATGCCCCGACGCGAGGATCTCGTCGTGACCCATG Gaps ö Score 1486; DB 2; Length 5874; 0; Indels Query Match 28.7%; Score 1486; Dest Local Similarity 100.0%; Pred. No. 0; Matches 1486; Conservative 0; Mismatches 3692 3752 2211 2091 3812 2151 3872 2331 4052 2391 4112 2451 4172 2511 4232 3932 3992 2271 g q a g ò 요 ò 셤 ò 셤 ò a ò 셤 ò ઠે 8 δ 8 WO9936562-A1

4352 GTGGCCGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTG 4411

2630

GCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACT 2631 GCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACT

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                                                                                                                                                                                                                                                                                                               The present invention describes a nucleotide expression system for the introduction of a therapeutic gene comprising: (1) a nucleotide sequence encoding an immune suppression gene; (ii) a promoter; and (iii) a transcription termination signal, where the system is able to inhibit, evade or eliminate a recipient cell immune response to the therapeutic gene when the gene is transformed into a recipient cell. AAX90481 to AAX90484 represent specifically claimed plasmid retroviral vector nucleotide sequences from the present invention. The expression system and vectors containing it can be used for gene therapy, for treating an MHC.I autoimmune disease or for killing tumour cells. The expression system contains an immunosuppressive gene which prevents host rejection of the vector
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                                                                                                                                                                                                                                                                                       Claim 25; Page 134-137; 154pp; English.
                                                                                                        (HUMA-) HUMAN GENE THERAPY RES INST.
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                                                                      98US-0071409P
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Matches 1486; Conservative
                                                                                                                                           Link CJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a nucleotide expression system for the introduction of a therapeutic gene comprising: (1) a nucleotide sequence encoding an immune suppression gene; (ii) a promoter; and (iii) a transcription termination signal, where the system is able to inhibit, evade or aliminate a recipient cell immune response to the therapeutic gene when the gene is transformed into a recipient cell. AAX90481 to AAX90484 represent specifically claimed plasmid retroviral vector nucleotide sequences from the present invention. The expression system and vectors containing it can be used for gene therapy, for treating an MHC-I autoimmune disease or for killing tumour cells. The expression system system contains an immunosuppressive gene which prevents host rejection
                                                        Plasmid retroviral vector; expression system; immunogenic; gene therapy; immune response; immunosuppression; gene delivery; therapeutic; MHC-I autoimmune disease; tumour; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression system containing therapeutic gene and an immunosuppressor gene useful for treating an MHC-I autoimmune disease or killing tumor cells.
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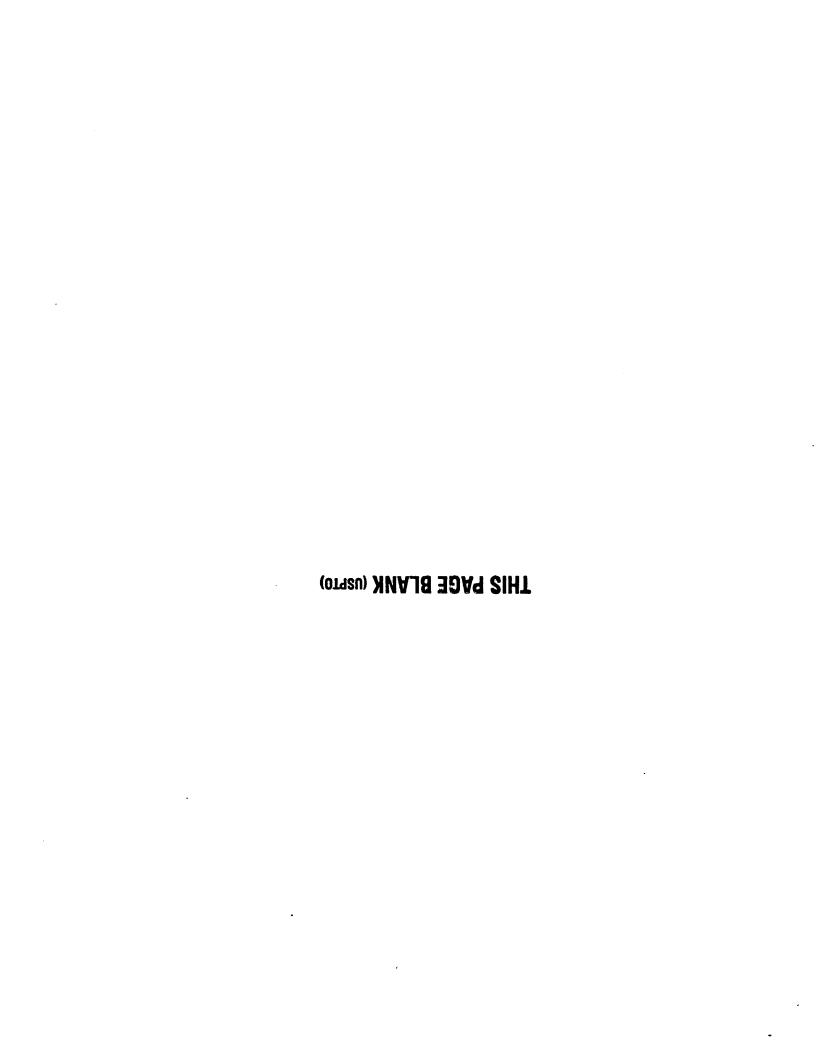
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant by comparison a humanised red shifted green fluorescent protein (HRGFP), and a promoter sequence and a termination sequence functionally coupled to the codding sequence. Also described: (1) a plasmid vector DNA sequence (II) anabling replication of the vector or in a host cell and (1); (2) infectious virus (III) comprising at least cell and (1); (2) infectious virus (III) and sequence from (I) in a host cell capable of the vector or in a host cell and (I); (2) infectious virus (III) and sorting at least one copy of (I). (I) is useful for identifying comprising at least one copy of (I). (I) is useful for identifying transformed cells to allow for direct observation of transferred genes into living cells to allow for direct observation of transferred genes into living cells by introducing (I) into the cell and measuring close into living cells which have been transferred cells. The catching the absorbance at 490-760 mm, and the excitation is from 420-470 mm. (I) is also useful for selecting sorter (FACS). The expression of the HRGFP gene in living cells with advance the study of gene transfer; gene expression and gene product function in vitro or in vivo, particularly for human gene therapy applications requiring FACS analyses of living cells. The present for applications requiring FACS analyses of living cells. The present capterions requiring FACS analyses of living cells. The present invention. N.B. The SEQ ID NO:8 in the sequence Listing represents a specification: where SEC ID NO:1 to 6 of the cequence Listing represent the sequence Listing represents and sequence Listing represents and sequence Listing represent the sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA construct for identifying transformed cells to allow for direct observation of transferred genes into living cells, comprising nucleotide sequence encoding red shifted green fluorescent protein.
                                                                                                                                                                                                                                                                                                                                                                 recombinant DNA construct;
humanised red shifted green fluorescent protein; HRGFP; fluorescence;
gene transfer; gene expression; gene therapy; bone marrow processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes a recombinant DNA construct (I)
4119 CTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGG 4164
                                                                                                                                                                                                                                                                                                         Plasmid vector pLESN nucleotide sequence SEQ ID NO:3
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                                                                                                                                         ADE82653 standard; DNA; 6620
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28.7%; Score 1486; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1486; Conservative 0; Mismatches
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4712 GGCCA 3797 GGCCA	_			4952 ATCAG 4037 ATCAG	5012 CACAA 4097 CACAA	5072 ATCCA 4157 ATCCA	5132 CTCCT 4217 CTCCT
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Search completed: February 27, 2006, 09:24:01 Job time : 2890 secs



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1: /cgn2_6/ptodats/1/pubpna/USOB_PUBCOMB.seq:*

3: /cgn2_6/ptodats/1/pubpna/USOB_PUBCOMB.seq:*

3: /cgn2_6/ptodats/1/pubpna/USOB_PUBCOMB.seq:*

4: /cgn2_6/ptodats/1/pubpna/USOB_PUBCOMB.seq:*

5: /cgn2_6/ptodats/1/pubpna/USOB_PUBCOMB.seq:*

6: /cgn2_6/ptodats/1/pubpna/USOB_PUBCOMB.seq:*

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9: /cgn2_6/ptodats/1/pubpna/USOB_PUBCOMB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-397-079-9
US-10-759-315-9
US-10-947-881-9
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US-09-252-656B-50
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                                                                                                                                                                                                                                                                           9793542 segs, 4134689005 residues
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US-11-036-557-9
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US-10-987-388-35
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US-10-164-965A-1
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Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-935-726-16	US-09-105-470-25	US-09-345-373-147	US-09-373-658-12	US-09-921-143-16	US-09-989-687-12	US-10-028-780-33	US-10-141-965-7	US-10-084-488-16	US-10-075-446-147	US-10-260-270-4	US-10-197-844-9	US-10-120-398-16	US-10-120-414-16	US-10-120-377-16	US-10-035-212-147	US-10-375-680-50	US-10-614-275-25	US-10-628-395-14	US-10-696-002-16	US-10-733-311-147	US-10-902-853-4
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ALIGNMENTS

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                                                           APPLICANT: Klaimea, Markku
APPLICANT: Klaimea, Markku
APPLICANT: Klaimea, Markku
APPLICANT: Lehtolainen, Pauliina
APPLICANT: Arriomaki, Varpu
APPLICANT: Arriomaki, Varpu
TITLE OF INVENTION: Biotin-Binding Receptor Molecules
FILE REPRENCE: GJE-48
CURRENT APPLICATION NUMBER: US/10/618,570
CURRENT APPLICATION NUMBER: US/09/622,804
PRIOR FILING DATE: 2002-12-10
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100.0%; Pred. No. 0;
:ive 0; Mismatches
Sequence 1, Application US/10618570 Publication No. US20040185059A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 5177; Conservative
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LOCATION: (1071)..(2270)
OTHER INFORMATION:
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LENGTH: 5177
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Sequence 14, Appl

Sequence

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	1801 AACTGITGAATAATACACTGAGGCTGAAGGATTGGGAACATTCTCAGACAT 1801 AACTGITGAATAATACACTAATGATCTGAGGCTGAAGGATTGGGAACATTCTCAGACAT 1801 AACTGITGAATAATAATACACTAATGATCTGAGGCTGAAGGATTGGGAACATTCTCAGACAT 1801 AACTGITGAATAATAATCACTTAATCACTGAGGCTGAAAGGGCTCGCTGACTGGGAAATGGACA 1911 CAAAAAATAATACACTTTACTCCAAGGTGCCCAGAAGTGCTCGCTGACTGGGAAATGGACACA 1921 ACGATCTGGGCTCCAACATGACCACTCGGGGCTGTGAACACGCCGCAGGCAAATCACAGGCAAATCACAGGCAAATGACACATGACACATGACACATCAGGGCACATCAGGGCACATCAGGGCACATCAGGGCACATCAGGGCACATCAACAGGCACATCAACAGGGCACATCAACAGGGCACATCAACAGGGCACATCAACAGGGCACATCAACAGGCCACATCAAAAAATCAAAAGAGTCACCACTGCATGGGAACTCAACAGGCACATCAACAGGGCCCAGCCAG	2221 2281 2281 2341
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	661 AGCAACTTATCHGTGTCGATTGTCTAGTGTCTTTTTTTTTT	1141 ATGCTCGCTCGCTTCGTTCCTCCCCATCCTAAAAATGGCCCAACTTCAAG 1200 1201 AGAGGAGGAGTTATAAAACTGCACTGCTCTTATCTCATGTGTTTGTAGTTC 1260 1201 AGAGGATGAAGTTATAAAACTGCACTGATCACCCTTTATCTCATTGTGTTTTGTAGTTC 1260 1201 AGAGGATGAAGTCTTATAAAACTGCACTGATCACCCTTTATCTCATTGTGTTTTGTAGTTC 1260 1201 AGAGGATGAAGTCGTATAAAACTGCACTCATAATCTCATTGTGTTTTGTAGTTC 1260 1261 TCGTGCCCATCATTGGCATAGTGGCAGCTCAGCTCCTGAAATGGGAAACGAAAAGAAATTGCA 1320

Db 1 TTTGAAGACCCCACCGTAGGTGGCAAGCTTAAGTAACGCACTTTGCAAGGCAT 60 Qy 61 GGAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGAACAAAGAAACGC 12 Db 61 GGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGAACAAAAAAAA	09 121 TGAATACCAACAGGATATCTGTGGTAAGGGGTTCCTGCCCCGGGTCAGGGCCAAGAACA 180	181 GATGAGACAGCTGAGTGATCCCCCGGGTCCAGCCTCAGCCCTCAGCGTTCTAGTGAACAGAACAGAAACAGAATGCTCCCCCGGGTCCCAGCCCTCAGCAGTTCTAGTGAA	Db 241 CTCGGGGCCAAGAACAGATGGTCCCCCAGAGGGCCCCCAGCCCTCAGCAGTTCTAGTGAA 300 Qy 301 TCATCAGATGTTTCCAGGGTGCCCCAAGAACACTGAAAATGACCCTTAGAAC 360	Db 301 TCATCAGATGTTTCCAGGGGCCCCAAGACCCTGAATGACCTTGTACTTTGAAC 360 Qy 361 TAACCAATCAGTTCCGCTTCTGTTCGCGCGCTTCCGCTCCCGAGCTCAATAAA 420	Db 361 TAACCAATCAGTTCGCTTCTGTTCGCGCGCTTCCGGTCTCCGAGTAAA 420 Qy 421 AGAGCCCACAAACCCTCACTCGGGGGGGGGGCGCTTTCCGATAGACTGCGTCGCGGGGTC 480	Db 421 AGAGCCCACACCCTCACTCGGGGGGCGCGTTTTCCGATAGATGGTGGTGGTGTGTTTTG 480 Qy 481 CCGTATTCCCAATAAAGCCTCTTGGTTTTGCATCGGGATCGTGGTGTTCCTTG 540	Db 481 CCGTATTCCCATAAAGCCTCTTGCTGTTCGACGACGTCTCGTTCGT	Db 541 GGAGGTCTCCTCTGAGTGATTGACTACCCACGAGGGGTCTTTCATTTGGGGGGTCTTC 600 Qy 601 CGGGGATTTGGAGACCCTGCCCAGGGACCCACCGACCACGGGAGGTGTAAGCTGGCC 660		dy 661 AGCAACTTATCTGTGTCTGCGATTGTCTATGTTTGATGTTTGATGTGTGGCCTGCG 720	Oy 721 TCGTACTACTAGCTAGCTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTT 780 1	Oy 781 CTGAACACCGGCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGCGCTTTTTGTGG 840	dy 841 CCCGACCTGAGGAAGCGAGTCGATGTGGAATCCGACCCCTCAGGATATGTGGTTCTGGT 900 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 901 AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGAA 960	Qy 961 CCGAAGCCGCGCGTTTGTCTGCTGCAGCTTGGGCTGCAGGTCGACGTCTAGAGGA 1020	Qy 1021 TCAATTCGGCACGAGTAAATCGCTGCTGCTGTTTAGGACATATGAAGTATGGCACAGT 1080	OY 1081 GGGATGACTTTCCTGATCAGCAAGAGACACTGACAGCTGTACAGAGTCTGGAAGTTCG 114
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2221 CTACCAGGGTCCAGCATCAACATCTCACTCGCCACACAGAGGAGTGAGT	3001 GCTTCAAATACCAGAACCATTTCAACTTCTTGGTTTTTAAGTGGCTCGTGCCGGAATTG 3060 2220 GTTGTCCTCTCGGAAATACACCTCCTTTCCATGGCTGCTGGGTGTGCTGCCCAACTGG 2279 3061 ATCCCCTCAGGATATAGTAGTTTTCGCTTTTGCATAGGGAAGTGGTGCTGCTGACTGG 2279 2280 ATCCCCTCAGGATATAGTAGTTTTCGCTTTTTGCATAGGGAAGGGGAAATGTAGTCTTATGC 3120 2280 ATCCCCTCAGGATATAGTAGTTTCGCTTTTTGCATAGGAAGGGGAAATGTAGTCTTATGC 2338 3121 AATACTCTTGTAGTCTTGCAACATGGTAACGATAGCAACATGCCTTACAAGGAGA 3180 2340 AATACCTTGTAGTCTTGCAACATGGTAACGATAGCAACATGCCTTACAAGGAGA 2399 3181 GAAAAAGCACCGTGCATGGTAACGATAGGTAAGTAGCAACATGCTTATTAGG 3240 2400 GAAAAAGCACCGTGCATGGTGAAGTAAGGTAAGTAGGATCGTGCCTTATTAGG 2459 3241 AAGGCAACAGGCGATGGCATTGGTGAAGTAAGGAATCGAATTCGCAATTACAGAATGAAT
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1111 ATGCTCGGTCAGTCAGTCTCCTCCCCATCCTAAAAATGGCCCAACTCTTCAAG 1200 1120 ACAGGTCTAGACTCTCTCCTCCTCCTCTAAAAATGGCCCAACTCTTCAAGTCC 179 1201 ACAGGTCTAGACTCTTATACTCCTTTATCTCATTGTTTTCTTC 1219 1201 ACAGGTCTAAAATGGCAAATGGCAAATGGCAAATGGCAATTGTTTTTTC 1219 1210 TGCTCGCTAATTGGCAATTGCTCACCAGTCTCTCTCCTCCAATTGTTTTTTTT	1735 TGGGGCTACTCCCTTAACTTCATGGGATATGGTAATTGGATGTGGGGC

OY 1621 CCACAGTACTTGATTTGCAGTTCAGTATTGAAACACTGAATGGCAGAGTCCAAGAGAATG	1681 CATTTAAACAACAAGGGGATGCGTAAATTAGAGG 1681 CATTTAAACAACAAGGGGGTGCGTAAATTAGAGGGGTGTGTGT	OY 1741 AAAITAAGTCTCTAGATGAAAACAAGTATATTTCGAACAGGAAATAAAAGGGGAAATGA 1 1 1 1 1 1 1 1 1	1801	1861	1921 1782	OY 1981 CCTACATCAGGCGGTAACAGCGCACATCAATGAGATCAAGAGTCACCACTGCGGA DD 1782TACTTTACCGCAAGAACATATTGTACTAAAAATCAAGCAATGTTTCG-	OY 2041 CACAAAACACCATCAACAAGAGCAGCCCACCTTTGGCTTCACCGTCAATTGGAAGT	Qy 2101 TTTCAGAGTCCACCACTGTCTTCACGGGCCAGTGCTTCATAGACAGGAAGGA	Qy 2161 TCCTGAAGACCATGTGGCTGCTGCGGTCAAGTGTTAATGACATTGGTGATGACTGGAAAG :	Oy 2221 CTACCAGGGTCGGCATCACATCTTCACTCGCCTGCGCACAGAAGGAGTGAGT	OY 2281 ACCAAGGTCCTCGTGGACTCCAGGTGAAAAGGAGATAGAGGCCCTCCTGGACAAATGG DD 2006 AACAATATCTGAACCTTTACCCGGTTGCCCGGCA	Qy 2341 TATACCAGGCTTTCCAGGTCTAATAGGTACTCCAGGTCTTAAAGGTGATCGGGGGGATCT Db 2040	OY 2401 CTGGTTTACCTGGAGTTCGAGGATTCCCAGGACCAATGGGGAAGACGGGAAGCCAGGAAC	Qy 2461 TTAATGGACAAAAAGGCCAGAAGGGAGAAAAAAGGGAGGAGGATGCAAAGACAATCTA 3 Db 2040ACGGTCAG 3	OY 2521 ATACAGTCGGACGGCGCGCCCTCACGAAGGCAGAGTGGAGATTTTTCACG 2 DD 2048 GTCTCTGCCAAGTGTTTGCTGACGCAACCCCCACTGGATGGGGTTGGCTATCGCCCATA 2	Oy 2581 AAGGCCAGTGGGGTGTGTGACGACGGCTGGAACTGCGTGGAGGACTGGTCGTCT 2 Db 2108 GCCGCATGCGCGGACCTTTGTGGCTCCTCTGCCG	2641 GCAGGAGCTTGGGATACAAAGG	Db 2142
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 2141 2700 2171

300 Abdoccrivity Abdoccrivity	RESULT 4 US-10-397-079-9 US-10-397-079-9 Sequence 9, Application US/10397079 Publication No. US20030224415A1 Sequence 9, Application No. US20030224415A1 Seturation No. US20030224415A1 APPLICANT: Bremel, Robert APPLICANT: Bremel, Robert TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors CURRENT APPLICATION NUMBER: US/10/397,079 CURRENT FILING DATE: 2003-03-26 SPRIOR APPLICATION NUMBER: US/09/897,511A PRIOR FILING DATE: 2000-06-29 PRIOR FILING DATE: 2000-07-03 NUMBER OF SEQ ID NOS: 36 SOFTWARE: Patentin Version 3.0 SEQ ID NO 9 LENGTH: 5130 TYPE: DNA
2701 GTACGGGTCCAATMTGGCTGAATGAAGTATTTTGTTTCGGGAAAGGGTCTCGGAAGGGTCTGAAGGGTCTGGAGGGTCTGAGTTTTTGTTTTTTTT	3476 GCTACTGGGCTATCTGGACAAGGGAAAACGCAAAGGGAAAGCAGGAAGTAGCTTGCA 3535 2700 GCTACTGGGCTATCTGGACAAGGGAAAACGCAAAGAGAAAGCAGAAGCAGTAGCTTGCA 2759 3536 GTGGGCTTACATGGCAAAAGGGAAAACGCAAAGAGAAAGCAGAACGGAAT 3595 2760 GTGGGCTTACATGGCGATAGCTAGGCGGTTTTATGGACAGCAAGCGAACGGAAT 2819 3596 GTGCCAGCTGGGAAGCTAAGGTTGGGAAGCCTTGAAGCAAAGCAAAGCAAAGCAACGAAT 2819 3596 TGCCAGCTGGGCGCCCTTGGTAAGGTTGGGAAGCCTGCAAAGTAAACTGGATGGCTT 3655 [

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4256 GCATGCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCA 4315 	දු දු	TAACCAATCAGTTCGCTTCTGCTTCGGTTCGGGGCTTCCGGTCTCCGAGCTCAATAAA
4316 TGGTGGAAAATGGCCGCTTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGGCGGAACC 4375	රු සි	421 AGAGCCACAACCCTCACTCGGCGCCCAGTCTTCCGATAGACTGCGTCGCCGGGTAC 480
GCTATCAGACATAGCGTTGGCTACTGATATTGCTGAAGAGCTTGGGCGGAATGGG GCTATCAGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGG [ර් සි	481 CCGTATTCCCAATAAAGCCTCTTGCTGTTTGCATCCGGAATCGTGGTCTCGCTGTTCCTTG 540
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ATCGCCTTCTTGACGACTTCTTCTGACGGGCTCTCGAGTTCGATA 4542 ATCGCCTTCTTGACGACTTCTTCTGACGGGACTCTCGAGTTCGATA 4542 ATCGCCTTCTTCTCACACTTCTTCTGACGGGACTCTCGAGTTCGATA 4542	ර් සි	601 CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCACCACCAGGAGGTAAGCTGGCC 660
	ර් යි	661 AGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTATGCGCCTGCG 720
equence 9, Application US/10759315 ublication No. US20040235173A1 EBREAL INPORMATION:	ò a	721 TCTGTACTAGTTAGCTAACTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTT 780
APPLICANT: Bremel, Robert D. APPLICANT: Miller, Linda U. TITLE OF INVENTION: Production of Host Cells Containing Multiple Integrating Vectors	<i>\$</i> 6	781 CTGAACACCCGGCACACACGGGACACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGG 840
CF INVENTION: DY SETTAL EFERENCE: GALA-08484 T APPLICATION NUMBER: US, T FILING DATE: 2004-01-1	& A	841 CCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT 900
SOFTWARE: Patentin version 3.2 EQ ID NO 9 ILENGIH: 5130	è a	901 AGGAGACGAGAACCTAAAACAGTTCCGCCTCCGTCTGAATTTTTGCTTTCGGTTTGGAA 960
Inte: DNA ORGANISM: FRATURE: OTHER INFORMATION: Synthetic 0-759-315-9	& 8	961 CCGAAGCCGCGCGTCTTGTCTGCAGCCAAGCTTGGGCTGCAGGTCGACTCTAGAGGA 1020
uery Match 30.7%; Score 1588.6; DB 8; Length 5130; est Local Similarity 66.1%; Pred. No. 0; atches 3007; Conservative 0: Mismatches 754; Indels 786; Gans 18;	<i>&</i> 8	1021 TCAATTCGGCAÇGAGTAAATCGGTGCTGCCGTCTTTAGGACATATGAAGTATGGCACAGT 1080
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Control Cont	& 8	1261 TCGTGCCCATCATTGGCATAGTGGCAGCTCCAGAATGGGAAACGAAACGAAGAATTGCA 1320
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Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION UNMBER: 60/215,851
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin version 3.0
SEQ ID NO 5130
                                                                                                                                                                             Query Match 30.7%;
Best Local Similarity 66.1%;
Matches 3007; Conservative (
                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Fublication No. US20050060762A1
GENERAL INFORMATION:
JAPPLICANT: Bleck, Gregory
ITILE OF INVENTION: Expression Vectors
FILE REPERENCE: GALA-06415
CURRENT APPLICATION NUMBER: US/10/947,881
CURRENT FILING DATE: 2004-09-23
PRIOR APPLICATION NUMBER: US/09/897,006
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                      Sequence 9, Application US/11036557
Publication No. US20050221429A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors Comprising in TITLE OF INVENTION: Amplifiable Marker
FILLE REFERENCE: GALA-09479
CURRENT APPLICATION NUMBER: US/11/036,557
CURRENT FILING DATE: 2005-01-14
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 9
LEAGHTH: 5130
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                                                                                                                                                                                                                                                                                                                       Score 1588.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 66.1%;
Matches 3007; Conservative
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28.7%; Score 1486; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1486; Conservative 0; Mismatches
                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
TELECOMMUNICATION INFORMATION
             TELEPHONE: 515-288-3667
TELEPAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 6620 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
TELECOMMUNICATION
TELEPHONE: 515.
TELEPAX: 515-27.
TYPE: NUCLEIC COLOGY: 11ne.
MOLECULE TYPE: 00
TYPOTHETICAL: NO
TYPOTHETICAL: NO
TYPOTHETICAL: NO
US-08-786-511B-3
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US-UB-786-511B-3

Sequence 3, Application US/0876651B

Publication No. US20020015979A1

GENERAL INFORMATION:

APPLICANT: Link, Charles J.

APPLICANT: Link, Charles J.

APPLICANT: Link, Charles J.

APPLICANT: Seregina, Tatiana

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Vehicles for Stable Transfer Stable Transfer Stable Transfer Stable States

STARE: Lova

COMPRESSEE: Zarley, McKee, Thomte, Voorhees & Sease

CONFOUTER: Lova

COMPUTER: Invention States

SOFTWARE: Popply disk

COMPUTER: Invention Bare: 21-JAN-1997

APPLICATION NUMBER: US/08/786,531B

FILING DATE: 21-JAN-1996

ATTORNEY/AGENT INFORMATION:

**REFERENCE/DOCKET NUMBER: 37,719

**REFERENCE/DOCKET NUMBER: BATTORNER: Patting

**REFERENCE/DOCKET NUMBER: BATTORNER: BA
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	Db 3737 CATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATG 3796 Qy 4712 GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATG 4771	Qy 4772 GAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCGGCTCAG 4831 Db 3857 GAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAG 3916 CC 4832 GGCCAAAAACAGAATGGTCCCCAAAACAGATCCTCTAAAACAAATAAAAAAAA	3917 GGCCAAGAACAGATGCTCCCCAGATGCGGCCTCAGCAGTTTCTAGAGAACCATC 4892 AGATGTTTCCAGGGTGCCCCAAGAACGACCTGAAATGACCTTATTTGAACTAACAA 3977 AGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCTGTGCCTTATTTGAACTAACAAAGACCTGAAATGACCTGTGCCTTATTTGAACTAACAAAGACCTGAAATGACCTGTGCCTTATTTGAACTAACAAAGAACCTGAAATGACCTGTGCCTTATTTGAACTAAACAAAAAAATGAACCTGTGCCTTATTTGAACTAAACAAAAAAATGAACCTGTGCCTTATTTGAACTAAACAAAAAAAA	Qy 4952 ATCAGTTCGCTTCTGGTTCGCGCGCTTCTGCTCCCGGGCTCAATAAAAGGCC 5011 bb 4037 ATCAGTTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCC 4096	4097 CACAACCCTCACTCTGGGGGCGCCAGTTCTCGATTGACTGGGTACCGTGTGGGGGGGG	CCTCTGAGTGATTGACTACCGGTCAGCGGGGGTCTTTCATTTGG 5177 [RESULT 10 US-10-164-965A-1 ; Sequence 1, Application US/10164965A ; Publication No. US20040001808A1 ; GENERAL INFORMATION: ; APPLICANT: Kenneth, Haglid ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE USE OF BCL-2 TRANSFECTED NEURONS; ; CURRENT APPLICATION NUMBER: US/10/164,965A ; CURRENT FILING DATE: 2002-10-22 ; NUMBER OF SEQ ID NOS: 11 ; SOFTWARE: Patentin version 3.1	; SEQ ID NO 1 ; LENGTH: 6046 ; TYPE: DNA ; ORGANISM: Human Bcl-2 transfected neurons US-10-164-965A-1	Query Match 28.6%; Score 1481; DB 6; Length 6046; Best Local Similarity 100.0%; Pred. No. 0; Matches 1481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 3697 GATCAAGAGACAGGATGGTTCGCATGATTGAACAAGATGGATTGCACGCAGGT 3756

1015 GTGCCGGGGCAGARTCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTRTCCATCATG 3364 1016 GTGCCGGGGCAGGARTCTCCTGTCATCACCTTGCTCTGCCCAGAAAAGTRTCCATCATG 3364 1016 GTGCCGGGGCAGGARTCTCCTGTCATCACCTCCTGCCCAGAAAGTRTCCATCATG 3364 1016 GTGCCGGGCGCTGCATACGCTTGATCCGGCTACCTCCCCATTCGACCACCACA 3424 1016 GTGCCGACACACCTCACCCAGAACTCTCGCCCACCCCATTCGACCACCACACACTGTCGCCCACCCCACCACCACACACTGTCCCCCACCCCCACCACCACACACTGTCCCCCCACCCCCACCCCCACCACACACA	S GACCTGAAATGACCTGTGCCTTATTTGACTAACCATTCGTTTTGTTTTGTTTG
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3348 AGAACAGTCCCCARAGGGGTCCCCCAGTTTTTTCAGGAACCATCAGATG 3407	Qy 3835 TTCCGGCTGTCGAGGGGCCCCGGTTCTTTTGTCAAGACCGACC

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US-10-359-397-1
'Sequence 1, Application US/10359397
'Publication No. US20040071673A1
'GENERAL INFORMATION:
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3715 GGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTG
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APPLICANT: Stratagene California
APPLICANT: Stratagene California
APPLICANT: Stratagene California
APPLICANT: Eraman, Jeffrey
APPLICANT: Carstens, Carsten-Peter
APPLICANT: Carstens, Carsten-Peter
APPLICANT: Bagga, Rajesh
APPLICANT: Campositions and Methods for Protein Isolation
ITILE OF INVENTION: Compositions and Methods for Protein Isolation
FILE REFERENCE: 25436/2465
CURRENT FILING DATE: 2004-11-12
PRIOR FILING DATE: 2003-11-13
PRIOR FILING DATE: 2003-11-13
FRIOR FILING DATE: 2003-11-13
SEQ ID NO 3:
LENGHARE: PatentIn version 3:1
LENGHARE: PatentIn version 3:1
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                   5177
                                                                                     RESULT 12
US-10-987-388-35
; Sequence 35, Application US/10987388
; Publication No. US20050158711A1
                                                                  GTCAGCGGGGTCTTTCATTTGG
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Best Local Similarity 100.
Matches 1463; Conservative
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SEQUENCE 3. Application US/10098035
| Sequence 3. Application No. US2002014198341
| GENERAL INFORMATION:
| APPLICANT: University of Southern California APPLICANT: Weiner, Leglie P. APPLICANT: Weiner, Leglie P. TITLE OF INVENTION: CONSTRUCTION AND USE OF GENES ENCODING TITLE OF INVENTION: PATHOGENIC EPITOPES FOR TREATMENT OF AUTOIMMUNE DISEASE FILE REFERENCE: 13761-703-00 US CURRENT FILING DATE: 2002-03-14
| PRIOR FILING DATE: 1996-05-29 | NUMBER OF SEQ ID NOS: 12 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 3 | LENGTH: 5865
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; OTHER INFORMATION: Sal/hind drag of pSVNA into Sal/Hind cut
US-10-359-397-1
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                  Genes
APPLICANT: University of Southern California
TITLE OF INVENTION: Construction and Use of Gene;
TITLE OF INVENTION: of Autoimmus Disease
FILE REFERENCE: 2013761-7030803001
CURRENT APPLICATION NUMBER: US/10/359,397
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: 10/098,035
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 1
SOUTHARE: Patentin version 3.1
                                                                                                                                                                                                                                               Query Match 28.1%; Score 1455.2; Best Local Similarity 98.4%; Pred. No. 0; Matches 1488; Conservative 0; Mismatches
                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial
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2872 AGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTG
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                                                                                                      4686 AGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTG
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Sequence 2, Application US/09808743

Patent No. US20020068711A1

GENERAL INPORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

APPLICANT: PEDERSEN, Peter

APPLICANT: PEDERSEN, Peter

TITLE OF INVENTION: ARREST OF PROLIFFATION OF HIGHLY GLYCOLYTI

FILE REFERENCE: JUL1720-1

CURRENT APPLICATION NUMBER: US/09/808,743

CURRENT FILING DATE: 2001-03-14

PRIOR PILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 10

SOUTHARE: Patentin version 3.0

SEQ ID NO 2:

LENGTH: 6444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Cloning vector pLXRN US-09-808-743-2
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                               FEATURE:
FOTHER INFORMATION: Retroviral vector derived from Moloney Murine
FOTHER INFORMATION: Leukemia Virus
FOTHER 10-098-035-3
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28.1%; Score 1455.2;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1488; Conservative 0; Mismatches
TYPE: DNA ORGANISM: Artificial Sequence
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2639 ATTGAACAAGATGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGGGTATTCGGC 2698 3790 TATGACTGGGCACAACAGAAATCGGCTGCTCTGATGCGCGGCTTTCCGGCTGTCAGCG 3849 2699 TATGACTGGGCACAACAGAATCGGCTGCTCTGATGCCGCGTTTCCGGCTGTCAGCG 2758 3850 CAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACTGTCCGGTGCCCTGAATGAA	GACGTTGTCACTGAGGGGAAGGGACTGGCTGTTGGGCGAAGTGCCGGGGCAGGAT 293 CTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGG 408 CTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGG 299 CTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGTGTTGTATCGATGCGG 299 CGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAAAATGCGATC 315 CGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAAAATGTGTT 101 CGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAAACATCGCATC 305			4510 GAGITCTICTGAGGGACTCTGAGGTTGATAAATTATTTATTTATTTAGG 4569 3419 GAGITCTICTGAGGGACTCTGGGGTTCGATAAATTATTTTATT	3599 ACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCC 3658 4750 GGCTCAGGGCCAAGAACAGATGGAACAGCTGATATCTGTGGTAAGCAGTTCCTGCCCC 3658 1619

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| cgn2 6/ptodate3/1/pubpna/USO9_NEW_PUB.seq:*
| cgn2 6/ptodate3/1/pubpna/USO9_NEW_PUB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 10, Appl Sequence 16, Appl	Sequence 2, Appli Sequence 16, Appl Sequence 1, Appli		Sequence 50, Appl Sequence 57, Appl Sequence 57, Appl Sequence 69, Appl	Sequence 74, Appl Sequence 61, Appl Sequence 66, Appl Sequence 69, Appl	34, 34,
SUMMARIES	US-11-205-031-10 US-11-233-119-16	US-10-948-344-2 US-11-053-187-16 US-10-523-682-1	US-11-082-154A-31 US-11-082-154A-118 US-10-525-710-66	US-10-525-710-65 US-10-525-710-65 US-10-525-674-57 US-10-525-710-69	US-10-525-710-74 US-10-525-674-61 US-10-525-674-66 US-10-525-674-69	US-10-525-710-79 US-11-053-187-17 US-10-933-746-34 US-11-071-651-15
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\$ Query Match Length DB	3974	2290 2403 2403	4323	5091 5091 5091 5860	5860 5860 5860 6472	6591 3906 5856 7448
% Query Match	22.6	222.6	2223	2000	2222	22.0 21.6 21.6 21.6
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3688 GATAGCTAGACTGGGCGGTTTTATGGACAGCAAGCGAACCGGAATTGCCAGCTGGGGCG 3629

3611 CCTCTGGTAAGGTTGGGAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCCAAGGA 3670

3551 GATAGCTAGACTGGGCGGTTTTATGGACAGCGAACCGGAATTGCCAGCTGGGGCGC 3610

3491 GGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGGTAGCTTGCAGTGGGCTTTACATGGC 3550

3748 GGACAAGGAAAACGCAAGCGCAAAGAAAGCAGGTAGCTTGCAGTGGGCTTACATGGC

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Sequence 10, Appl	Sequence 1, 1	Sequence 22, Sequence 33.	Sequence 27,		Sequence 29,	Sequence 31,	Sequence 34,	Sequence 23,	Sequence 24,	Sequence 25,	Sequence 30,	Sequence 3,	Sequence 1	Sequence 100,	Seguence 13,	Semience 16	Sequence 15,	Sequence 44,	Sequence 39,			DB 12; Length 3974; 268; 1; Indels 0; Gaps 0;	AAGCTTCACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAAGGAAGG		AGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGGATGAATGTCAGGTACTGGGGTATCT 3490	
12 US-11-193-750	12 US-11-231-725-1	12	17	12 US-11-186	7 5	12	12	17	2 5	1 5	17	12	7	۲ ۱	- 6	1	12	12	12 US-11-180	ALIGNMENTS 1. cation US/11205031 US20050287588A1 FION: Et al. Et al. TION: Breast Cancer Specific Gene PR342D1 ATION WUBBR: US/11/205,031 CON NUMBER: US 09/017,715 TE: 1998-02-03 TE: 1998-02-03 TE: 1997-02-03	on 3.1	.9%; Score 1170.4; .9%; Pred. No. 8.7e- e 0; Mismatches	ccecaagcacTcagggcgcaagg	CCGCAAGCACTCAGGGCGCGAAGG	gcagaaacggrgcrgaccccgga	
1089.6 21.0 623	21.0	18.8	18.7	970.2 18.7 2716	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.5	16.7	16.5	16.4	16.1	16.4	16.4 1	849.8 16.4 12604 849.8 16.4 14561	5-031-10/c ee 10, Apl ation No. i INFORMAN TANT: 11 OP INVEW TY TAPPLICAT APPLICATI PILING DI	F SEQ ID SEQ ID 10 3974 NA W: Homo 8	atch cal Similarity 1171; Conservat	3371 AAGCTTCACGCTG	3868 AAGCTTCACGCTG	3431 AGAAAGCCAGTCC	
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us-10-618-570-1.rnpbn

CURRENT FILING DATE: 2005-09-23 PRIOR APPLICATION NUMBER: 09/107,997 PRIOR FILING DATE: 1998-06-30 PRIOR FILING DATE: 1998-06-30 PRIOR FILING DATE: 1998-06-30 PRIOR FILING DATE: 1999-10-13 PRIOR PILING DATE: 1997-12-24 PRIOR PLING DATE: 1997-12-24 PRIOR PLING DATE: 1997-16-06 PRIOR PLING DATE: 1997-06-06 PRIOR PLING DATE: 1994-03-08 NUMBER OF SEQ ID NOS: 35 SOFTWARE PATENTIN VERSION 3.0 SEQ ID NO 16 LENGTH: 3974 TYPE: DNA ORGANISM: Expression vector PHEA4-5 FEATURE: NAME/KEY: misc_feature LOCATION: (1)(3974) COTHER INPORMATION: Expression vector PHE4-5 US-11-233-119-16	Query Match 22.6%; Score 1170.4; DB 12; Length 3974; Best Local Similarity 99.9%; Pred. No. 8.7e-268; Matches 1171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Oy 3371 AAGCTTCACGCTGCCGCAAGCACTCAGGCCGCAAGGGCTGCTAAAGGAAGCGGAACACGT 3430	Oy 3431 AGAAAGCCAGTCCGCAGAACGGTGCTGACCCCGGATGAATGTCAGCTACTGGGCTATCT 3490	Oy 3491 GGACAAGGAAAACGCAAAGGAGGAAAGCAGGTAGCTTGCAGTGGGCTTACATGGC 3550 	0y 3551 GATAGCTAGACGCGGTTTTATGGACAGCAAACCGGAATTGCCAGCTGGGGCGC 3610	0y 3611 CCTCTGGTAAGGTTGGGAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCCAAGGA 3670	Oy 3671 TCTGATGGCCAGGGGATCAAGATCTGATCAGAGGATGAGGATGACGTTTCGCATGA 3730	0y 3731 TTGAACAAGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCT 3790	0y 3791 ATGACTGGGCACAACAGCAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGGGC 3850	0y 3851 AGGGCCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAA	0y 3911 ACGAGGCGGCGCTATCGTGGCCACGACGGGCGTTCCTTGCGCCACTGTGCTCG 3970 bb 3328 ACGAGGCGGGGCTATCGTGGCCACCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
Db 3628 CCTCTGGTAAGGTTGGAAGCCCTGCAAGATCGATGGCTTTCTTGCCGCCCAAGAA 3569 Oy 3671 TCTGATGGCGCGGGGATCAAGATCTGATCAAGAGCTTTCTTGCCGCCCAAGAA 3730 Db 3568 TCTCATGGCGCGGGGATCAAGATCTCAAGAGAAGGATCGGTTCGCTTCGCTTGATTCGCTTA 3730 Oy 3731 TTGAACAAGATGGATTGCACGCAGGTTCTCCCGCCGCTTGGGTGGAGACGTTTCGCTTA 3509 Oy 3731 TTGAACAAGATGGATTGCACGCAGGTTCTCCCGGCCGCTTGGGTGGAGAGCTATTCGGCT 3790 I	OY 3971 ACGITGICACIGAAGGGAAAGGGACIGGCTGCIATIGGGCGAAGIGCCGGGGCAGGAIC 4030 	OY 4031 TCCTGTCATCTCACCTTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGC 4090	Qy 4091 GGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCCAGGGGAAACATCGCATCG 4150	Oy 4151 AGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCGACGAAGAGC 4210	Oy 4211 ATCAGGGGTCGCGCCAACTGTTCGCCAGGCTCAAGGGGGGATGCCCGACGGG 4270	OY 4271 AGGATCTCGTCGTCGATGCCATGCCGGTTGCCGAATATCATGGTGGAAAATGGCC 4330	Qy 4331 GCTITICIGATICALCACUTGGCCGGCTGGGTGGCGGACCGCTATCAGGACATAG 4390 Db 2908 GCTITICIGGATICALCGACTGGGCCGGCTGGGGTGGGGGCGGCCGTATCAGGACATAG 2849	Oy 4391 CGTTGGCTACCGTGATATTGCTGAAGAGTTGGGGGGGGAATGGGCTGACCGCTTCCTCG 4450	Oy 4451 TGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCTTCTTCTATCGCCTTCTTGACG 4510	Oy 4511 AGTICTICTGAGCGGACTCTGGGGTTCGATA 4542 	RESULT 2 US-11-233-119-16/C ; Sequence 16, Application US/11233119 ; Publication No US20060025331A1 ; GENERAL INPORMATION: ; APPLICANT: HU, JING-SHAN et al, ; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2 ; FILE REFERENCE: PF112P4D1 ; CURRENT APPLICATION NUMBER: US/11/233,119

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8560 TGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACG 8619
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7540 AGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCAGCTACTGGGCTATCT
                                                     GGACAAGGGAAAACGCAAAGCGCAAAGAGAAAGCAGGTAGCTTGCAGTGGGCTTACATGGC
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Publication No. US20060013805A1

GENERAL INFORMATION:

APPLICANT: Lin, Y.

APPLICANT: Lin, Y.

APPLICANT: Lin, Y.

APPLICANT: Lin, Y.

CURRENT HILNG DATE: 2004-09-23

PRIOR APPLICATION NUMBER: US/10/948,344

CURRENT APPLICATION NUMBER: US/09/865,022

PRIOR APPLICATION NUMBER: US/09/865,022

PRIOR FILING DATE: 2001-05-24

PRIOR FILING DATE: 1999-11-24

PRIOR FILING DATE: 1999-11-24

PRIOR FILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO. 2
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US-10-523-682-1

Sequence 1, Application US/1053682

Sequence 1, Application US/1053682

Publication No. US20060014149A1

GENERAL INFORMATION:
METHODE FOR THE PROBLEM OF THE PROBLEM OF TITLE OF INVENTION:
TITLE OF INVENTION: Methods for rolling circle amplification and signal trapping of TITLE OF INVENTION: Inbraries

FILE REFERENCE: 10292.204-US

CURRENT APPLICATION UNDERF: US/10/523,682

CURRENT FILING DATE: 2005-02-01

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.3

SEQ ID NO 1

LENGTH: 2403
1510 GCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGAACGAAGAGCA 1451
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                                                                                                                                                                            CCTGTCATCTCACCTTGCTCCTGCCGAGAAGTATCCATCATGGCTGATGCAATGCGGCG
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                                                                                                                                      CCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCG
                                                                                                                                                                                                               GCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGA
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Best Local Similarity
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                                                                                                                              APPLICANT: INVITROGEN CORPORATION
APPLICANT: CHESNUT, Jonathan D.
APPLICANT: SHUMAN, Stewart
APPLICANT: SHUMAN, Stewart
APPLICANT: HENMAN, Stewart
APPLICANT: HENMAN, John A.
APPLICANT: HENMAN, John A.
APPLICANT: BENNETT, Robert P.
TILE OF INVENTION: METHODS AND REAGENTS FOR MOLECULAR CLONING
FILE REFERENCE: INVITI300-1
CURRENT FILING DATE: 2005-02-07
PRIOR FILING DATE: 2005-02-07
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
SPRIOR FILING DATE: 2000-08-21
SOFTWARE: Patentin Version 3.0
SOFTWARE: Patentin Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.6%; Score 1167.8; DB 12; Length 2290; 99.8%; Pred. No. 2.8e-267; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: pUni/V5-His version A vector
US-11-053-187-16
                                                                             ; Sequence 16, Application US/11053187; Publication No. US20050282184A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial sequence
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Pred. No. 8e-264;
0; Mismatches 1; Indels
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Rewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 17084-02203 (420C)
CURRENT APPLICATION NUMBER: 05/11/082,154A
CURRENT FILING DATE: 2005-03-15
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-05-31
PRIOR FILING DATE: 2002-05-31
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
SPRIOR FILING DATE: 2002-05-30
SPRIOR FILING DATE: 2002-05-30
SPRIOR FILING DATE: 2002-05-30
SOFTWARE: PABLESCO FOR WINDOWS VERSION 4.0
SEQ ID NO 31
LENGTH: 9136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: pWE15 cosmid vector
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank X65279
DATABASE ENTRY DATE: 1995-04-14
                                                                                                                          , Sequence 31, Application US/11082154A
, Publication No. US20060024820A1
, GENERAL INFORMATION:
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22.3%;
Best Local Similarity 99.8%;
Matches 1166; Conservative (
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                                                                                                      US-11-082-154A-31/c
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Pred. No. 1.2e-263;
0; Mismatches 1; II
PRIOR APPLICATION NUMBER: US 10/161,403
PRIOR FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 118
LENGTH: 17384
                                                                                                                                                                                                                                ; OTHER INFORMATION: pFK161 Plasmid US-11-082-154A-118
                                                                                                                                                                                                                                                                                                       Query Match 22.3%;
Best Local Similarity 99.8%;
Matches 1166; Conservative (
                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                           GGCAGCGCGCGCTATCGTGGCCTGCCCACGACGGCGTTCCTTGCGCAGCTGTGCTCGACGT
                                                                                                                                                                                                           GGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCCAGCTGTGCTCGACGT
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| Publication No. US20060024820A1
| GENERAL INFORMATION:
| APPLICANT: Perkins, Edward
| APPLICANT: Greene, Amy
| APPLICANT: Greene, AMP
| APPLICANT: Greene, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCTGAGCGGGACTCTGGGGTTCGATA 4542
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US-11-082-154A-118/c
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Sequence 58, Application US/10525674
Publication No. US20060003425A1
GENERAL INFORMATION:
APPLICANT: Kolperoge, Corinna
APPLICANT: Kolperoge, Corinna
APPLICANT: Harwig
APPLICANT: Hafner, Stefan
APPLICANT: Hafner, Stefan
TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
TITLE OF INVENTION: Sulphur (Meta)
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                      CTGGATGGCTTTCTTGCCGCCAAGGATCTGATGGCGCAGGGGATCAAGA
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                                                                    GACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGC
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US-10-525-710-66

J Sequence 66, Application US/10525710

Publication No. US2005060721A1

GENERAL INFORMATION:

APPLICANT: Zelder, Oskar

APPLICANT: Schroder, Hartwig

TITLE OF INVENTION: WHERE: 2005-02-24

PRIOR FILING DATE: 2005-02-24

PRIOR PLILOR DATE: 2002-08-26

PRIOR PLILOR DATE: 2002-08-26

PRIOR PLILOR DATE: 2002-08-26

NUMBER OF SEQ ID NOS: 79

SOFTWARE: Patentin version 3.3

SEQ ID NO 66

LENGTH: 4323
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                                                                                                                                                                                                               GGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCT
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                                                                       TCTCGTCGTGACCCATGCCGATGCCTGCTTGCCGAATATCATGGTGGAAAAATGGCCGCTT
                                                                                                                   TTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGACCGCTATCAGGACATAGCGTT
                                                                                                                                                 TTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGGCCGTATCAGGACATAGCGTT
                                                                                                                                                                                         GGCTACCCGTGATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCT
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US-10-525-710-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

22.0%; Score 1136.4; DB 8; Length 4323;
Best Local Similarity 99.9%; Pred. No. 1.1e-259;
Matches 1137; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                     CTTCTGAGCGGGACTCTGGGGTTCGATA 4542
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APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Corinna
APPLICANT: Zelder, Oskar
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Hafner, Stefan
TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
TITLE OF INVENTION: Sulphur (metY)
FILE REFERENCE: 13111-00006-U3
CURRENT APPLICATION NUMBER: US/10/525,710
CURRENT APPLICATION NUMBER: DCT/EP 2003/009453
PRIOR FILING DATE: 2003-08-26
PRIOR PLING DATE: 2003-08-26
PRIOR PLING DATE: 2003-08-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.3
SEG ID NO 65
LENGTH: 5091
                                                                                                                                                                                                                                                                                                                                CGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCG 2438
                                                                                                                                                                                                                                                                                                   CGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCG 4484
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                     2139 CGATCAGGATGATCTGGACGAACGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAG
                                                                                             GCTCAAGGCGCGCATGCCCCGACGGCGAGGATCTCGTCGTCGTGACCCATGGCGATGCCTGCTT
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Pred. No. 1.2e-259;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 65, Application US/10525710; Publication No. US20050260721A1; GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 1137; Conservative 0
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US-10-525-710-65
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US-10-525-674-58
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FILE REFERENCE: 13111-00002-US
CURRENT APPLICATION NUMBER: US/10/525,674
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: PCT/EP 2003/009452
PRIOR APPLICATION NUMBER: DE 102 39 073.8
PRIOR PILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: DE 102 39 073.8
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.3
SEQ ID NO 58
                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                 Score 1136.4; DB 8;
Pred. No. 1.2e-259;
0; Mismatches 1;
TITLE OF INVENTION: Sulphur (Meta)
CURRENT PAPLICATION NUMBER: US/10/525,674
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: PCT/FP 2003/009452
PRIOR APPLICATION NUMBER: PCT/FP 2003/009452
PRIOR APPLICATION NUMBER: DE 102 39 073.8
PRIOR APPLICATION NUMBER: DE 102 39 073.8
PRIOR PILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.3
SEQ ID NO 57
LENGTH: 5091
                                                                                                                                                                                                                                                                                                                 22.0%;
                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity '99.9'
Matches 1137; Conservative
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US-10-525-674-57
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APPLICANT: Zelder, Oskar
APPLICANT: Solpproge, Corinna
APPLICANT: Schroder, Hartwig
APPLICANT: Hafner, Stefan
TITLE OF INVENTION: Method for Zymotic Production of Pine Chemicals Containing
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Publication No. US20050260721A1
GENERAL INFORMATION:
APPLICANT: Zelder, Oskar
APPLICANT: Schpprogge, Corinna
APPLICANT: Schroder, Hartwig
APPLICANT: Hafner, Stefan
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APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Corinna
APPLICANT: Calder, Oakar
APPLICANT: Calder, Corinna
APPLICANT: Schroder, Hartwig
APPLICANT: Hafner, Stefan
APPLICANT: Hafner, Stefan
TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
TITLE OF INVENTION: Sulphur (metY)
FILE REFERENCE: 13111-0006-US
CURRENT APPLICATION NUMBER: US/10/525,710
CURRENT APPLICATION NUMBER: PCT/EP 2003/009453
PRIOR PLILNG DATE: 2005-08-26
PRIOR PPLICATION NUMBER: DE 102 39 082.7
PRIOR PLILNG DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 69
LENGTH: S860
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                                                                                                                                                                                                                                                                                                                                                                                                                        , Sequence 69, Application US/10525710
; Publication No. US20050260721A1
; GENERAL INFORMATION:
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Best Local Similarity 99.9°
Matches 1137; Conservative
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APPLICANT: Kroger, Burkhard

APPLICANT: Zelder, Oskar

APPLICANT: Zelder, Oskar

APPLICANT: Zelder, Oskar

APPLICANT: Zelder, Hartwig

APPLICANT: Schroder, Hartwig

APPLICANT: Hafner, Stefan

TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing

TITLE OF INVENTION: Wholes: Us/10/525,674

CURRENT APPLICATION NUMBER: Us/10/525,674

CURRENT FILING DATE: 2005-02-24

PRIOR PLILING DATE: 2003-08-26

PRIOR PLILING DATE: 2003-08-26

PRIOR APPLICATION NUMBER: DE 102 39 073.8

PRIOR PLILNG DATE: 2002-08-26

NUMBER OF SEQ ID NOS: 69

SOFTWARE: Patentin version 3.3

SEG ID NO 61

LENGTH: 5860
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                                                                                                                                                 2492 GCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCGTCGTGACCCATGGCGATGCCTGCTT
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Best Local Similarity 99.9%;
Matches 1137; Conservative (
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TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing TITLE OF INVENTION: Sulphur (metY)
FILE REPERBERGE: 13111-00006-045
CURRENT APPLICATION NUMBER: US/10/525,710
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: PCT/EP 2003/009453
PRIOR FILING DATE: 2003-08-26
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.3
SEQ ID NO 74
LENGTH: 5860
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ORGANISM: Artificial sequence
FEATURE:
COTHER INFORMATION: Description of the artificial sequence: plasmid
US-10-525-710-74
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APPLICANT: Hafner, Stefan
TITLE OP INVENTION: Method for Zymotic Production of Fine Cher
TITLE OP INVENTION: Sulphur (Meta)
FILE REPERBORS: 13111-00002-US
CURRENT APPLICATION NUMBER: US/10/525,674
CURRENT FILING DATE: 2005-02-04
PRIOR FILING DATE: 2005-08-26
PRIOR FILING DATE: 2003-08-26
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.3
SEQ ID NO 66
LENGTH: 5860
                                                                                                                                             TYPE: DNA ORGANISM: Artificial sequence
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                                              CTGGATGGCTTTCTTGCCGCCCAAGGATCTGATGGCGCAGGGGATCAAGATCTGATCAAGA
                                                                        GACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCCGGC
                                                                                    GACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCCGGC
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US-10-525-674-66
Sequence 66, Application US/10525674
Sepulication No. US20060003425A1
GENERAL INFORMATION:
APPLICANT: Kroger, Burkhard
APPLICANT: Kolpprogge, Corinna
APPLICANT: Solder, Oskar
APPLICANT: Schroder, Hartwig
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ò	2512 GACAATCTAATACAGTCCGACTGGTGGGTGGCAGCCCTCACGAAGGCAGAGTGGAGA 2571	0y 3587 AACC	AACCGGAATTGCCAGCTGGGGCCCCTCTGGTAAGGT GTGCACATGCTTTTACATGTGTTTTAGTCGAGGTTAAAA
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Other;plasmid DNA
phiBMDN-NSA: 5'LTR (position 1-1159); y+ (position
1160-1640); HisD (position 1641-2928), Myo-D NSA ApaI fragment
(position 2929-4389); driving neo (position 4390-5259); with 3'LTR
(position 5260-5964); Figures 8A-8C.
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                                                                                                                                                                                                  Score 1661.6; DB 2; Length
Pred. No. 0;
0; Mismatches 1641; Indele
                                                                                                                                                                                                  Query Match 32.1%;
Best Local Similarity 61.1%;
Matches 3536; Conservative 0
              LENGTH: 8316 base pairs
TYPE: NUCLEIC ACID
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: Ocher; plasmi
DESCRIPTION: pLHDWDN-NSA:
DESCRIPTION: 1160-1640);
                                                                                                                                 DESCRIPTION:
DESCRIPTION:
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REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: FHCR-1-5789
TELECOMMUNICATION INFORMATION:
TELECHOME: 1-206-682-8100; 1-206-224-0727 (direct)
TELEFRAX: 1-206-224-0779
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; Beguence 4, Application US/07753520B
; Patent No. 5352595
; GENERAL INFORMATION:
    APPLICANT: Tapscott, J.; Weintraub, H.M.; Palmer, T.D.
; TITLE OF INVENTION: "MyoD REGULATORY REGION"
    NUMBER OF SEQUENCES: 4
    CORRESPONDENCE ADDRESSS:
    ADDRESSEE: Christensen, O'Connor, Johnson and Kin STREET: 2800 Pacific First Center, 1420 Fifth Ave.
    STREET: Washington
    STATE: Washington
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ZIP: 98101-2347
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb stc
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/753,520B
FILING DATE: 19910903
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: none
FILING DATE: none
RILING DATE: none
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TELEX: 4938023
INFORMATION FOR SEQ ID NO:
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CAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT
                                                                                               AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAA
                                                                                                                          AAGCAGTTCCTGCCCCCGCTCAGGCCCAAGAACAGATGGAACAGCTGAATATGGGCCCAAA
                                                                                                                                                     CAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCCAAGAACAGATGGTCCCCCA
                                                                                                                                                                     CAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCA
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                                                                    CAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/09380190A
Patent No. 6410220
GENERAL INFORMATION:
APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: PCT/US98/03918
ATPLING DATE: 28-FEB-98
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REFERENCE/DOCKET NUMBER: 33,977
TELECOMMUNICATION INFORMATION:
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ADDRESSE: MUETING, RAASCH & GEBHARDT,
STREET: 119 NORTH FOURTH STREET, SUITE
CITY: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
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APPLICATION UNMERS: US/09/380,190A
FILING DATE: 26-Aug.1999
CLASSIFICATION: <UNKnown>
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                  Score 1629.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (Genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 29: US-09-380-190A-29
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 5594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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98.6%;
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Matches 1654; Conservative
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                                                                                                                                                                                                                           DB 3; Length 5130;
                                                                                                                                                                                 754; Indels
                                                                                                                                         Score 1588.6;
Pred. No. 0;
0; Mismatches
  ; LENGTH: 5130
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-511A-9
                                                                                                                                         Query Match
Best Local Similarity 66.1%;
Matches 3007; Conservative
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APPLICANT: Bremel, Robert
APPLICANT: Bremel, Robert
APPLICANT: Miler, Linda
APPLICANT: Miler, Linda
APPLICANT: Miler, Linda
APPLICANT: Miler, Cells Containing Multiple Integrating Vectors
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
FILE REFERENCE: GALA-06416
CURRENT APPLICATION NUMBER: 00/09/997,511A
CURRENT FILING DATE: 2000-07-03
RIOR PRIOR PLING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOPTWARE: Patentin version 3.0
SEQ ID NO 9
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Patent No. 6852510
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US-09-897-511A-9
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승 염	961 CGGAAGCCGCGCTTTGTTGCTGCAGCCAGCTTGGGCTGCAGGTCGACTCTAGAGGA 1020	2 A	1830AAAACTGCCTGTAAATAGACCTATTGATTGGAA
ð í	TCAATTCGGCACGAGTAAATCGGTGCTGCCGTCTTTAGGACATATGAAGTATGGCACAGT	<i>ት</i> ብ	2101 TITCAGAGICCACCACTGICTCACGGGCCAGIGGITC
8 8	1021 CC	8 8	2161 TCCTGAAGACCATGTGGCTGCTGCGGTCAAGTGTTAAT
ል ይ	1060 AGGACCCCTGCTCGTGTTACAGGCGGGTTTTTCTTGTTGAAAGAATCCTCACATACC 1119	3 &	2221 CTACCAGGGTCGGCATCAACATCTTCACTCGCCTGCGC
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8		පි සි	2281 ACCAAGTCCTCCTGGACTCCAGGTGAAAAGGAGATA 1
à à	1180 TGGCCAAAATTCGCAGTCCCCAACCTCCAATCACTCACCACTCTTGTTGTCTTG 1239	ò	2341 TATACCAGGCTTTCCAGGTCTAATAGGTACTCCAGGTC
S 8	TCCTGGCTATC	qa	2040
ò	ATCTCCAAGTCCGGAAGGCAAAGGAAATGGCAGTG	ර් ර	2401 CTGGTTTACCTGGAGTTCGAGGATTCCCAGGACCAATG
QQ	1277 ATATICCTCTTCATCCTGCTGTGTCTTCTTGTTGGTTCTTCTGGACTACCAA 1336	9 2	2040
ò	aagatgaaatgagatttcgagaagctgtgatggaacgcatgagcaacatggaagcagaa	g 23	
අු	GGTATGTTGCCCGTTTGTCCTCTACTTCCAGGAACATCAACTACCAGGACCAA	ò	2521 ATACAGTÇÇGACTGGTGGGTGGCAGCGGCCCTCACGAA
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qq	1509 CAAGATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCGG	3 8	GTACGGGTCCAATATGGCTGA
ð 1	CCACAGTACTTGATTTGCAGTTCAGTATTGAAACACTGAATGGCAGAGTCCAAGAGAATG	qa	2172
3 8	1550 -CICAGIIIACIAGIGCCAIIIGIICAGIGGIICGIAGGGCIIICCCCCACIGIIG 1605	Š	2761 AGTGCAGAATTAGACAGTGGGGGTGTGAGAGCCTGTTCG
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qq	1665 CCTTTTACCTCTATTACCATTTTCTTTTGGGTATACATTTAAACCCTAATAA 1724	3 8	2881 ATTTTTCCTTTGCTTCACTAAAATCAGCTTAATTAA
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9	1/82IACITIACCGCAAGAACAIAITGIACIAAAAAICAAGCAATGITITCG- 1829		

ACTGCGTGGAGGACTGGTCGTCT 2640-TTGGCTTCACCGTCAATTGGAAGT 2100 ATATTTAAGAAACTAAGAATTTT 2940 ACATATAAAATAGCTTCATATTT 3000 GAGGGGGAAATGTAGTCTTATGC 3120 CATAGACAGGAATGGGAAGGAGG 2160 ATCCTGCCTTAATGCCTTTATAT 1944 TGACATTGGTGATGACTGGAAAG 2220 SCACACAGAAGGAGTGAGTG 2280 AACTTACAAGGCCTTTCTGTGTA 2005 AGAGGCCCTCCTGGACAAATGG 2340 CTTAAAGGTGATCGGGGGGATCT 2400 GGGGAAGACCGGGAAGCCAGGAC 2460 STGGAAGCATGCAAAGACAATCTA 2520 AGGCAGAGTGGAGATTTTTCACG 2580 sardeedcridecrareeccara 2107 ----- 2141 TAAGCGAGCTTATTTTGGAAAAG 2700 CGGGAAAGAGTCATCCATTGAAG 2760 GCACGACGAAGATGCTGGGGGTC 2820 GCTCGCAGGCGGTCTGGAGCGAA 2197 ATTITITAAACTGTTATAAAGTG 2880 1959 ------ACGGTCAG 2047 ACTCCTAGCAGCTTGT----- 2171 ------ 2171 ------ Accadacter 2219 TTTAAGTGGCTCGTGCCGAATTG 3060

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APPLICANT: Link, Charles J.
APPLICANT: Link, Charles J.
APPLICANT: Levy, John P.
APPLICANT: Levy, John P.
APPLICANT: Bergins, Suming
APPLICANT: Seregins, Tatiana
TITLE OF INVENTION: Vehicles for Stable Transfer of Green
TITLE OF INVENTION: Pluorescent Protein Gene and Methods of Use for Same
TOTHE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Zarley, McKee, Thomte, Voorhees & Sesse
                                                                                                                                                                                                                             3542 GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATG 3601
   CCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATA 3481
                                                                                                      GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATG
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                                                                   CATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATG
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COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYES: Floppy disk
COMPUTER: IBM FC compatible
OPERATURS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,531B
FILING DATE: 21-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/010371
PILING DATE: 22-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NABER: 37,719
REGISTRATION NUMBER: 37,719
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STREET: 801 Grand Suite 3200
CITY: Des Moines
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Avenue
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| Patent No. 5352595 |
| GENERAL INFORMATION: |
| APPLICANT: Tapscott,J.;Weintraub,H.M.;Palmer,T.D. |
| TITLE OF INVENTION: "MyoD REGULATORY REGION" |
| NUMBER OF SEQUENCES: 4 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSE: Christensen, O'Connor, Johnson and Kind |
| STREET: 2800 Pacific First Center, 1420 Fifth Aven |
| STATE: Washington |
| STATE: Washington |
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ZIP: 98101-2347
COMPUTER READABLE FORM:
COMPUTER: TYPE: Diskette-5.25 inch, 1.2Mb of the computible operating system: MS-DOS 4.01
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/753,520B
FILING DATE: 19910903
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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                                                                                                                                                                                                                                            28.7%; Score 1486; D
100.0%; Pred. No. 0;
ive 0; Mismatches
 REFERENCE/DOCKET NUMBER: hgtri
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-280-367
TELEPHONE: 515-280-367
TELEPACK: 515-280-138
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERIFORS:
LENGTH: 6620 base pairs
TYPE: nucleic acid
STRANBEDNESS: 8ingle
TYPE: nucleic acid
STRANBEDNESS: 1inear
NOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 1486; Conservative
                                                                                                                                                                               HYPOTHETICAL: N
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US-08-786-531B-3
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Sequence 3, Application US/08654737B

Facent No. 6274136

Farent No. 62741379

Farent Reference: 13761-703-00 US

FARENT FILING DATE: 1996-05-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SERVIT: 5865

TYPE: DNA
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      GTGGCCGGCTGGGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTG
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                                                                                                                                                                                                                                                              DESCRIPTION: DLHDMDN-53: 5'LTR (position 1-1159); Y+ (position 159-1640); HisD (position 1641-3007); Myo-D 531.4 Apal fragment DESCRIPTION: 1159-1640); HisD (position 1641-3007); Myo-D 531.4 Apal fragment DESCRIPTION: (position 3008-5248); driving neo (position 5249-6117); with a DESCRIPTION: 3'LTR (position 6118-6823) coupled to a pBR322 plasmid (position US-07-753-5208-3
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100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels 0
FILING DATE: none
ATTORNEY/AGENT INFORMATION:
NAME: Sundsmo_John, 2.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: FHCR-1-5789
TELECOWUNICATION INFORMATION:
TELECHOME: 1-206-682-8100; 1-206-224-0779
TELEFAX: 1-206-682-8100; 1-206-224-0779
TELEFAX: 1-206-224-0779
TELEFAX: 4938023
INFORMATION ON SEQ 10 NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 9115 base pairs
TYPER: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                 MOLECULE TYPE: Other; plasmid DNA
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Matches 1486; Conservative
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                                   GCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTC
                                                                         AGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTG
                                                                                            AGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTG
                                                                                                                                    CCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGT
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                GCCATTTTGCAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTC
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APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate I
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
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CITY: Wayne
STATE: New Jersey
COUNTR: Wayne States
COUNTR: United States
ZIP: 07470-8426
COMPUTER: READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPERATING SYSTEM: PC-DOS/MS-DOS
SOPERATING SYSTEM: PC-DOS/MS-DOS
SOPERATING SYSTEM: DC-DOS/MS-DOS
SOPERATING SYSTEM: PC-DOS/MS-DOS
SOPERATING PATE: 05-UN-1995
CILASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .v-462-859A-6; Sequence 6, Application US/08462859A; Patent No. 5652092; GENERAL INFORMATION: Application US/08462859A;
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                                                                                                                     Gaps
            FEATURE:
OTHER INFORMATION: Retroviral vector derived from Moloney Murine
OTHER INFORMATION: Leukemia Virus
                                                                                                                   21;
                                                                                       Length 5865
                                                                                                                                                3687 ATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAA
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                                                                                       DB 3;
                                                                                    Score 1455.2; Pred. No. 0; 0; Mismatches
                                                                                      Query Match
28.1%;
Best Local Similarity 98.4%;
Matches 1488; Conservative
ORGANISM: Artificial Sequence
; ORGANISM: Art:
; FEATURE:
; OTHER INFORMAN;
; OTHER INFORMAN
US-08-654-7378-3
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US-08-48-28-39-48

1.85-quence 8, Application US/08462859A

Patent No. 5652092

GENERAL INPORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STATE: New Jersey
CCUNTRY: United States
INITY: Wayne
STATE: New Jersey
CCUNTRY: United States
INITY: ONE COMPATE: Floppy disk
COMPUTER: EMP FC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-UUN-1995
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       5771 GAACTGCAGGACGAGCGCGCGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCA
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                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                 Score 1448.4;
Pred. No. 0;
0; Mismatches
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEPAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.5%;
Matches 1474; Conservative
                                                                                            LENGTH: 8591 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                TOPOLOGY: circular

MOLECULE TYPE: CDNA

FEATURE:
NAME/KEY: CDS

LOCATION: 2393..3868
US-08-462-859A-6
                                                                                                                                                                                                          CDS 2393..3868
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Sequence 6, Application US/08123659A

Sequence 6, Application US/08123659A

Parent No. 5656477

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Of B-Amyloid Peptide
TITLE OF INVENTION: of B-Amyloid Peptide

TITLE OF INVENTION: Of B-Amyloid Peptide

CORRESPONDENCE ADDRESS:
ADDRESSER: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212

COUNTRY: U.S.A.

STATE: New York

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                    4080
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GCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCG
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                                                                                                                 GAACTGCAGGACGAGCGCGGCGTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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US-08-123-659A-6
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                                                                                                                                                                                                                                                                                                                                     Score 1448.4;
Pred. No. 0;
0; Mismatches
                                                                      31,844-04
             ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,084
REFERENCE/DOCKET NUMBER: 31,844
TELECOMMUNICATION INFORMATION:
TELEFAX: (201)831-3246
TELEFAX: (201)831-3365
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 8591 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.5%;
Matches 1474; Conservative C
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6250 CAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGAC
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIPICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: ROSENDlum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (518)475-0611
TELEPAX: (518)475-0611
INFORMATION FOR IN ON: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8591 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                    Score 1448.4;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.5%;
Matches 1474; Conservative
                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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2393..3868
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. LOCATION:
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"18-08-464-247A-6

Sequence 6, Application US/08464247A

Sequence 6, Application US/08464247A

Patent No. 569347

GENERAL INFORMATION:

APPLICANT: Jacobsen, J. S.

APPLICANT: Vitek, M. P.

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation

TITLE OF INVENTION: of B-Amyloid Peptide

NUMBER OF SEQUENCES: 19
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   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFFATION NUMBER: 33,43
ATTORNEY/AGENT INFORMATION:
NAME: ROSenblum, Anne M.
REGISTRATION NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEC 10 NO: 8:
LENGTH: 8591 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: CDS
NAME/KEY: CDS
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larity 99.5%; Pred. No. 0;
Conservative 0; Mismatches
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; LOCATION:
US-08-123-659A-8
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Matches 1474;
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                                                                GCTGGGGCCCCCTCTGGTAAGGTTGGGAAGCCCTGCAAGTAAACTGGATGGCTTTCTTG
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Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen,
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                                               SIKEET: ONE CAMPUS DITOE

CITY: Paraippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAITHARG, Blizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.0%; Score 1448.4;
llarity 99.5%; Pred. No. 0;
Conservative 0; Mismatches
                    Company
                  ADDRESSEE: American Cyanamid
STREET: One Campus Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8591 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
CORRESPONDENCE ADDRESS:
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Matches 1474; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-08-464-247A-6
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APPLICANT: Vitek, M. P.

TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESSES:
CORRESSES: American Cyanamid Company
STREET: One Campus Drive
CITY: Paralippany
STRIET: One Campus Drive
CITY: Paralippany
STRIET: New Jersey
COUNTRY: United States
ZIPME: New Jersey
CONPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUMRENT APPLICATION NUMBER: US/08/464,247A
ATTORNEY/AGENT INFORMATION:
NUMBER: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,688
REGISTRATION SOCKET NUMBER: 31,788
REGISTRAT
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TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: cDNA
FEATURE:
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US-08-464-247A-8
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                                                               5351 TGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAAGCGGAAAGCCAAGCGCTACCAGTGGG
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              GCTGGGGCGCCCTCTGGTAAGGTTGGGAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTG
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 <u>CGGAACACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCAGCTAC</u>
                                                 CTTACATGGCGATAGCTAGACTGGGCGGTTTTATGGACAGCAAGCGAACCGGAATTGCCA
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Pred. No. 0;
0; Mismatches 6;
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Best Local Similarity 99.5%;
Matches 1474; Conservative (
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STRANDEDNESS: double
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2393..3868
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US-08-464-248A-6
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AC157118 Bos tauru
CQ830753 Sequence
CS104130 Sequence
AJ966780 Synthetic
X05343 Chicken mRN
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AJ616762 Synthetic
L27818 Gallus gall
AJ311647 Gallus ga
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AX926677 Sequence
D13381 Oryctolagus
L11692 Oryctolagus
AF203781 Mus muscu
D13362 Mus sp. mRN
L04274 Mus musculu
BC003814 Mus musculu
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C122N15/09, A61K48/00, A61P43/00, C07K14/705//A61K38/00, C12N15/00,
A61K37/02
Strandedness: Single;
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CQ722728 Sequence
172357 Sequence 3
AR270697 Sequence
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E03268 cDNA sequen
E05211 DNA encodin
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E03267 cDNA sequen
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BD000148 Antihuman
D90187 Homo sapien
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X51689 B.taurus mR
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23-FEB-1998 GB 9803757.5,24-JUN-1998 GB 9813653.4 PI
YLA HERTTUALA, MARKKU KULOMAA, PAULIINA LEHTOLAINEN, VARPU I
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Herttuala,S.Y., Kulomaa,M., Lehtolainen,P., Marjomaki,V. and
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Biotin-binding receptor molecule
Patent: JP 2002504328-A 1 12-FBB-2002;
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CC Topology: Linear; CC Biotin-binding receptor molecule FH Key Location/Qualifiers In 10712270. FEATURES In 1517 And Lype="genomic DNA" Anignment Scores: Alignment Alignment A	Db 1071 HIGH	Qy 61 PheValValLeuValProlleileGly11eValAlaAlaGlnLeuLeuLy8TrpGluThr 80 Db 1251 TTTGTAGTTCTCGTGCCCATCGTTGGCATAGTGGCAGCTCTGAAATGGAAACG 1310 Qy 81 Ly8AbanCy8ThrValGlySerValAsnAlaAspIleSerProSerProGluGlyLy8Gly 100 Db 1311 AAGAATTGCACGTTGGCTCAGTTAATGCAGATATATCTCCAAGTCCGAAAGGCAAAGGA 1370 Qy 101 AsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsnMet 120 Qy 101 AsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsnMet 120 Db 1371 AATGGCAGTGAAGATGAGATTTCGAGAAGTGTGTGATGAGCAACATG 1430	Qy 121 GluserargileGlnTyrLeuseraspasnGlualaasnLeuLeuAspalaLysasnPhe 140 Db 1431 GaAaGCAGATCCAGTATCTTTCAGATAATGAAGCCAATCTCTAAGAATTTC 1490 Qy 141 GlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsnSer 160 Db 1491 CAAAATTTCAGCATAACAACTGATCAAAGATTTAATGATGTTCTTTTCCAGCTAAATTCC 1550 Qy 161 LeuLeuSerSerIleGlnGluHisGluAanTTAATGATGTTCTTTTCCAGCTAAATTCC 1550 Db 1551 TTACTTTCCTCCAGGAACATGAGAATATCATAGGGGATATCTCCAAGTCATAGTA 1610 Qy 181 GlyLeuAsnTrTtvvalLeuAspLeuAspLeuAspLeuAspLaatCATAGGAATATCAAGAGTCATAGTA 1610 Qy 181 GlyLeuAsnTrTtvvalLeuAspLeuAspLeuGlnPheSerIleGluThrLeuAsnGGYARGYA 1670 Db 161 GlyLeuAsnTrTtvvalLeuAspLe	201 GINGLUASANTAPAELYSGINGLUGUNMETATGLYSLEGGGUGLUATGILETYTASAN	Qy 241 GlyGluMetLysLeuLeuAsnAsnleThrAsnAsnAspleuArgLeuLysAspTrpGluHis 260 Db 1791 GGGAAATGAAACTGTTGAATAATATCACTAATGATCTGAGGCTGAAGGATTGGGAACAT 1850

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CAAGAGAATGCATTTAAACAACAAGAGAGAGATGCGTAAATTAGAGGAGGGTGTAATACAAT
                                                                                                                                                                                                      GGGGAAATGAAACTGTTGAATAATATCACTAATGATCTGAGGCTGAAGGATTGGGAACAT
                           LeuleuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeuVal
                                                                     GlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArgVal
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SM Unknown.
Unclassified.
(CE 1 (bases 1 to 1807)
ORS Krieger,M. and Kodama,T.
S Scavenger receptor protein and antibody thereto
RNAL Patent: US 5510466-A 1 23-APR-1996;
Massachusetts Institute of Technology; Cambridge, MA
Location/Qualifiers
1807
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Sequence 1 from patent US 5510466.
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US-10-618-570-2 (1-400) x BTSCAVR1
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/tissue type="lung"
/clone Tib="lzAPII"
22. 1383
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ThrileGlyAlaValAsnSerArgGlyGluPheThrGlyThrTyrIleThrAlaValThr 310
                                           TACTCCAGGTCTTAAAGGTGATCGGGGGATCTCTGGTTTACCTGGAGTTCGAGGATTCCC 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (07-AUG-1990) Krieger M., Massachusetts Institute of
Technology, Room E25-236, 77 Massachusetts AVe, Cambridge MA 02139,
U S A
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1 (bases 1 to 1592)
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                                                                                                                                                                                                                                                                                                                                                                                                 macrophage scavenger receptor type I; membrane
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                                                                                    AlaThrSerAsnGluIleLysGluSerProLeuHisGlyThrGlnAsnThrIleAsnLys
                                                                                                                                                                                                                  1052 AAAAGGGAG------100AAGCATGCAAAGACC 1078
                                                                                                                                                                           331 ArgThrGlnProThrPheGlyPheThrValAsnTrpLysPheSerGluSer 347
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scavenger receptor type
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Matches:
Conservative:
Mismatches:

    1592
    organism="Bos taurus"
|mol_type="mRNA"
    db_xref="taxon:9913"

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macrophage
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lipid metabolism; m
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Direct Submission
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Score:
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Bos taurus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
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                                                                                                                                                                                                                                                                        GTGAAGTTCGATGCTCGCTCAGTGACAGCTTTGCTTCCTCCCCATCCTAAAAAATGGCCCA
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                                                                                                                                                                   21 VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro
                                                                                                                                                                                                                                                                                                                                              41 ThrLeuGlnGluArgMetLysSerTyrLysThrAlaLeuIleThrLeuTyrLeuIleVal
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                                                                                                                                 MetalaGlnTrpAspAspPheProAspGlnGlnGluAspThrAspSerCysThrGluSer
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180 575 200 635

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Cough, P. J., Greaves, D.R. and Gordon, S.
Gough, P. J., Greaves, D.R. and Gordon, S.
Direct Submission
Submitted (08-DEC-1997) Sir William Dunn School of Pathology, South
Parks Road, Oxford OX1 3RE, England
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP037351 11-JUL-2001
Homo sapiens macrophage scavenger receptor type III (SR-A) mRNA,
complete cds.
AF037351. GI:3004959
                                                                                                                                                                                                                                                                                                                                                             241 GlyGluMetLysLeuLeuAsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGluHis 260
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 1167)
Gough, P.J., Graaves, D.R. and Gordon, S.
A naturally occurring isoform of the human macrophage scavenger receptor (SR-A) gene generated by alternative splicing blocks modified LDL uptake
J. Lipid Res. 39 (3), 531-543 (1998)
                                     141 GlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsnSer
                                                                                                                                                                                                  GlnGluAsnAlaPheLysGlnGlnGluGluMetArgLysLeuGluGluArglleTyrAsn
  GAAAGCAGAATCCAGTATCTTTCAGATAATGAAGCCAATCTCCTAGATGCTAAGAATTTC
                                                              CAAAATTTCAGCATAACAACTGATCAAAGATTTAATGATGTTCTTTTCCAGCTAAATTCC
                                                                                                                                              TTACTTTCCTCCATCCAGGAACATGAGAATATCATAGGGGATATCTCCAAGTCATTAGTA
                                                                                                                                                                                                                                                                                                                      636 CAAGAGAATGCATTTAAACAACAAGAGGAGATGCGTAAATTAGAGGAGCGTATATACAAT
                                                                                                                        LeuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeuVal
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/function="blocks modified LDL uptake"
/note="isoform; normal alternative splice product"
/note="isoform; normal alternative splice product"
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/produci="macrophage scavenger receptor type III"
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/cell_type="monocyte"
1. .1167
/gene="SR-A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 SerGlnThrLeuLysAsnIleThrLeuLeuGlnGly 272
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/organiam="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="8"
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1. .2135
/ organism="Bos taurus"
/ organism="Bos taurus"
/ db_xref="taxon:9913"
/ clone="pBKS1"
/ tissue_type="nung"
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LLSSIQEHBKITODISKSLVCLNTTVLDLOFSIETLNGRVQENGRTKEERI
YNASABIKSLDEKQVYLEQEIKGEMKLLANITNDLRLKDWEHSQTLKNITLLQGPPGP
PGEKGDRGPPGCDNGIPGFPGLIGTPGLKGDRGISGLPGVRGFPGEPMGKTGKPGLNGGK
GQKGEKGSGSMQRPG"
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                                                                                                                                                                                                Submitted (07-AUG-1990) Krieger M., Massachusetts Institute of Technology, Room E25-236, 77 Masachusetts AVe, Cambridge MA 02139, U S A
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                1 (bases 1 to 2135)
Robrer, L., Freeman, M., Kodama, T., Penman, M. and Krieger, M.
Colled-coil fibrous domains mediate ligand binding by macrophage
scavenger receptor type II
Nature 343 (6258), 570-572 (1990)
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        MetAlaGlnTrpAspAspAspPheProAspGlnGlnGlnGluAspThrAspSerCysThrGluSer

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Pecora, Bovidae, Bovinae, Bos
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Krieger, M.
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anti-sense: No;
*source: cell_type
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87.2%
72.2%
50.6%
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E03268
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                                                                                                           Homo sapiens (human)
                                                                                                 JP 1991290184-A/2.
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PPGEKGDRGPTGESGPRGFPGPIGPPGLKGDRGAIGFPGSRGLPGYAGRRGNGCPKG
KGEKGSGNTLSTGPIMLNEVFCFGRESSIEECKIRQMGTRACSHSEDAGVTCTL"
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                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, 1 (Dases, Homo.)

1 (Dases 1 to 1347)

Matsumoto, A. and Kodama, T.

CELL OF SCAVENGER RECEPTOR-PRODUCING ANIMAL PARAMACEUT CO LIA 2 19-DEC-1991;

CHUGAI FHARMACEUT CO LIA 2 19-DEC-1991;

CHUGAI FARAMACEUT CO LIA 2 10-DEC-1991;

CHUGAI FARAMACEUT CO LIA 2 10-DEC-1991;

CHUGAI FARAMACEUT CO LIA 2 10-DEC-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PhevalvalleuvalProllelleGlyIleValAlaAlaGlnLeuLeuLysTrpGluThr 80
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47. .1123
/product='human scavenger receptor,type II'
1124..1301.
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                                                                                                  human scavenger receptor, type II
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197
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*Bource: cell_line=THP-1;
Key
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Matches:
Conservative:
Mismatches:
Indels:
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MATSUMOTO AKIYO, KODAMA TATSUHIKO
C12NS/10,C12N1S/12,C12Q1/06;
Btrandedness: Single;
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nic RNA"
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    .1347
    /organism="Homo sapier/mol_type="genomic RNJ/db_xref="taxon:9606"

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PAT 31-JAN-2002
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Gaps:
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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                                    GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn 119
                                                                                                             MetGluSerArgIleGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139
                                                                                                                                  SerbeuleuSerSerlleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerbeu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsnAlaSerAlaGluIleLysSerLeuAspGluLysGlnValTyrLeuGluGlnGluIle 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysGlyGluMetLysLeuLeuAsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGlu 259
AAGAATTGCTCAGTTAGTTCAACTAATGCAAATGATATAACTCAAAGTCTCACGGGAAAA 346
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-1991 JP 1991229728
7-AUG-1990 JP 990 222339
KODAMA TATSUHIKO, MATSUMOTO AKIYO, SUZUKI HIROSHI PC
1/08,GOIN33/53,GOIN33/577//A61K39/395,A61K39/395,C12N5/20,
                                                         TTCCAAAATTTCAGCATGACAACTGATCAAAGATTTAATGACATTCTTCTGCAGCTAAGT
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1 (bases 1 to 1347)
Kodama,T. Matsumoto,A. and Suzuki,H.
ANTI-HUMAN SCAVENGER RECEPTOR ANTISODY
Patent: JP 1993192179-A 2 03-AUG-1993;
CHUGAI PHARMACEUT CO LTD
OS Homo sapiens (human)
PN JP 1993192179-A/2
PD 03-AUG-1993
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receptor I
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/organism="Homo sapiens"
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JP 1993192179-A/2. Home sapiens (human)
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(C12P21/08,C12R1:91);
strandedness: Double;
topology: Linear;
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PN UP
PD 03-7-1
PR 27-1
PR 27-1
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C12P21/OD
C12P1/OD
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                               OS Homo sapiens (human)
PN JP 2000312595-A/2
PN JP 2000312595-A/2
PD 14-NOV-2000
PP 14-APR-2000 JP 2000114233
PR ITASUHIKO KODAMA, AKIYO MATSUMOTO, HIROSHI SUZUKI PC
C12N15/09, C07KL6/28 (C12N5/10, C12P21/08// (C12N5/10, C12R1:91), PC
(C12P21/08, C12R1:91), C12N15/00, C12NS/00, (C12N5/00, C12R1:91) CC
FH Key Location/Qualifiers
I : .10 Coganism='Homo sapiens (human)'.
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Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                    Hominidae, Homo.

1 (bases 1 to 1347)

Kodama,T., Matsumcto,A. and Suzuki,H.
Antihuman scavenger receptor antibody
Patent: JP 2000312595-A 2 14-NOV-2000;
CHUGAI PHARM CO LTD
    Antihuman scavenger receptor antibody
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                           BD000149.1 GI:18623228
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1042.50
87.2%
72.2%
50.6%
                                    JP 2000312595-A/2.
Homo sapiens (human)
Homo sapiens
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Best Local Similarity:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleo
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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PE Corporation (NY) (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression patent: US 6500938-A 1260 31-DEC-2002;
Incyte Genomics, Inc.; Palo Alto, CA;
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Sequence 1260 from patent US
AR270697 GI:29701931
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Unclassified.
In (bases 1 to 1367)
S Iveko, P.G., Elshourbagy, N.A. and Brawner, M.E. Attachment enhanced 293 cells
AL Patent: US 5683903-A 3 04-NOV-1997;
Location/Qualifiers
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Matches:
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/organism="unknown"
/mol_type="unassigned
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Sequence 3 from patent
I72357
I72357.1 GI:3008496
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Shinjuku-ku, Tokyo 162
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1 (bases 1 to 1367)
                                                                             Homo sapiens (human)
                                                         GI:219991
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307 AAGAATTGCTCAGTTAGTTCAACTAATGCAAATGATATAACTCAAAGTCTCACGGGAAAA 366
                                                                                                                                                                                                                                                                                                                                                                                                  GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn 119
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KGEKGSGNTLRPVQLTDHIRAGPS"
HUMPHSR2 1367 bp mRNA linear PRI 18-DEC-2002 Homo sapiens phSR2 mRNA for scavenger receptor type II, complete
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Mateumoto, A., Naito, M., Itakura, H., Ikemoto, S., Asaoka, H.,
Hayakawa, I., Kanamori, H., Aburatani, H., Takaku, F., Suzuki, H.,
Kobari, Y., Miyai, T., Takahashi, K., Cohen, H.E., Wydro, R.,
Hugoman, B.D. and Kodama, T.
Human macrophage scavenger receptors: primary structure,
expression, and localization in atherosclerotic lesions
Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9133-9137 (1990)
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Indels:
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Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Homo.

1 (bases 1 to 2028)
Matsumoto, A. and Kodama, T.
CELLO F SCAYROGER RECEPTOR-PRODUCING ANIMAL
PATENTE: JP 1991290184-A 1 19-DEC-1991;
CHUGAI PHARMACEUT CO LTD
OS Homo sapiens (human)
PN JP 1991290184-A/1
PD 19-DEC-1991
PP 06-APR-1390 JP 1990090274
PI MATSUMOTO AKIYO; KODAMA TATSUHIKO
PC C12N5/10, C12N15/12, C12Q1/06;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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791.5
748.5
736.5
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719.5
717
714.5
688.5
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669.5
665
664
 Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/Abss/ABSS/MEB ppool/109106136570/runat 27022006 063856 13092/app_query.fasta_1
-O=/Abss/ABSS/MEB ppool/109106136570/runat 27022006 063856 13092/app_query.fasta_1
-DB=EST -QFWT=fastap -SUFFIX=rst -MINATCH=0.1 -LGOPCL=0 -LGOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-UNTFATT=pto -NORM=ext -HEAPSIZES=500 -MININEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=USI0618570 @CGN 1 1 5315 @runat 27022006 063856 13092 -NCPU=6 -ICPU=3
-NO MMAP -NG SCÖRES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                              ; Search time 5148 Seconds (without alignments) 3635.360 Million cell updates/sec
                                                                                                                                                                                    MAQWDDFPDQQEDTDSCTES.....DWKATRVGINIFTRLRTQKE 400
                                                                                                                                                                                                                                                                                                                                    82156650
             GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                   nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                       41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                 of hits satisfying chosen parameters:
                                                                                                February 27, 2006, 09:14:37
                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                              Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
                                                                                                                                                       US-10-618-570-2
2059
                                                                                                                                                                                                                BLOSUM62
                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                Scoring table:
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Total number

Searched:

Minimum DB Maximum DB

hdmn131_h hdm004_h1 603764104

AK089178 RW956649 BW956649 BW956649 BW008649 CCB469554 CCB469554 CCB991736 BW408647 BW268637 CCB98183 BW408648 BW409120 CCB98175 BW958294 BW9582332 BW958294 BW4569 CCC69175 CCC691795 CCCC691795 CCC691795 CCC691795 CCC691795 CCC691795 CCC691795 CC

603158328 603958787 603232324

hdm005_e1 hdmn128_h

603212130 603158704 BX269637

BN50 B10. AGENCOURT hdm003_c0 4037151_1 pgp2n.pk0 pgn1c.pk0 ur33b12.y

hdm004 d0 Controle

LPSC_K10 LPSd_K03 UI-M-GV0-

LPSm_G16 Controle LPSi_014 603957428

ALIGNMENTS

RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_est2:*
gb_est3:*
gb_est5:*
gb_est5:*
gb_est6:*
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gb_est6:*
gb_est6:*
gb_est7:*
gb_gss2:*

gb_est1:*

EST: *

Database

SUMMARIES

DNS48862 1407127 M CP409555 CH3#061_D AY413208 HOMO BAPI CB453082 708007 MA AY413209 Pan trogl CN641776 ILLUMIGEN BX496563 DKFZp779D

DN548862 CF409555 AY413208 CB453082 AY413209 CN643776 BX496563

949 1033 652 1027 978 843

555.4 499.5 455.9

1276 1140.5 1042.5 1020 1002.5 944.5 885

264667

Description

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Query Match Length

Score

Š.

Result

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The Bases 1 to 949)

Stry 1, Desai,R., Olarte,M., Henthorn,P. and George A.L.

Expressed sequence tags from Canine heart
Unpublished (2003)
Other_ESTS: CH3#061_D06MR
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2660
Email: al.george@vanderbilt.edu
Insert Length: 2287 Std Error: 0.00
Seq primer: Mr: GTTTTCCCAGTCACACGTTG
High quality sequence start: 169
High quality sequence stop: 784.
                       CHAUGH DOGME Canine heart normalized CDNA Library in pBluescript Canis familiaris CDNA clone CH3#061_D06 5', mRNA sequence.
                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /notes Organ: heart; Vector: pBluescript; Site_1: 5' of vector Not1; Site_2: 3' of vector EcoR1; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"
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Matches:
Conservative:
Mismatches:
Indels:
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1. .organism="Canis familiaris"
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                                                                              CF409555.1 GI:34410801
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94.8%
55.4%
                                                                                                         familiaris (dog)
                                                                                                       Canis familiaris
Canis familiaris
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Query Match:
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     RESULT 2
CF409555
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole embryos."
                                                                                                                                                                                                                                                                      MetAlaGlnTrpAspAspPheProAspGlnGluAspThrAspSerCysThrGluSer
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                                                                                        21 ValLysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro
                                                                                                                                                                             41 ThrLeuGlnGluArgMetLy8SerTyrLysThrAlaLeulleThrLeuTyrLeulleVal
1 MetalaGlnTrpAspAspPheProAspGlnGlnAspThrAspSerCysThrGluSer
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Av413208.1 GI:39769173
                                                                      AsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsnMet 120
                                                                                                                          140
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                                                                                                                                                                                                                                                                                                                       GinGluAsnAlaPheLysGinGluGluMetArgLysLeuGluGluArgIleTyrAsn 220
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1 (Dases 1 to 1033)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                               624
                                                                                                                                                                                    625 CAAAATTTCAGCATAACAACTGATCAAAGATTTAATGATGTTCTTTTCCAGCTAAATTCC 684
                                                                                                                                                                                                                                                                         GlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArgVal 200
                                                                                                                                                                                                                                                                                      Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
LysAsnCysThrValGlySerValAsnAlaAspIleSerProSerProGluGlyLysGly
                                         AAGAATTGCACGGTTGGCTCAGTTAATGCAGATATATCTCCCAAGTCCGGAAGGCAAAGGA
                                                                                                                      GluSerArgileGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsnPhe
                                                                                                                                               GAAAGCAGAATCCAGTATCTTTCAGATAATGAAGCCAATCTCCTAGATGCTAAGAATTTC
                                                                                                                                                                                                                        LeuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeuVal
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/organism="Homo sapiens"
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Matches:
Conservative:
Mismatches:
Indels:
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Query Match:
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141 GlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsnSer 160
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1 (bases 1 to 1027)
Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Textiars, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pan troglodytes MSR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                              121 GluSerArgIleGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsnPhe
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/locus_tag="HCM4814"
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1 (bases 1 to 652)

2 Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

3 Second set of bovine ESTS from pooled-tissue normalized libraries (npublished (2003)

3 Contact: Smith TPL

4 USDA, ARS, US Weat Animal Research Center

6 Dex 166, Clay Center, NE 68933-0166, USA

7 Tel: 402 762 4366

Fax: 402 762 4366

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                                                                             EST 26-MAR-2003
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/incte="vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/inclary made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pitultary, and
placenta/endometrium."
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Mismatches:
Indels:
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Query Match:
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Macaca mulatra Macaca mulatra Eukaryota; Mammalia; Buteleostomi; Mammalia; Butheria; Buarchoncoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

1 (bases 1 to 978)
Magness, C. L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Magness, C.E., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. al Iadonato, S.P.
Analysis of the Macaca mulatra transcriptome and the sequence divergence between Macaca and human divergence between Macaca and human Genome Biol. 6 (7), R60 (2005)
                                                                                                                                                                                                                  Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA
Tel: 2063780400
                                                                                                                                                                                                                                                                                                                    FORWARD: CCCTCACTAAAGGGAACAAAA
BACKWARD: CACTATAGGGCGAATGGGTA
INSERT Length: 978 Std Error: 0.00
Plate: CL000089 row: C column: 03
Seq primer: CCCTCACTAAAGGGAACAAAA
                                                                                                                                                                                                                                                                          Email: cmagness@illumigen.com
Sequenced on 2004.01.16. 752 Q20
PCR PRimers
                              Macaca mulatta (rhesus monkey)
                                                                                                                                                                                                                                                                Fax: 2063780408
CN643776.1
EST.
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DB:
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KEYWORDS
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AUTHORS
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            Length:
Matches:
Conservative:
Mismatches:
                                                                                 Gaps:
                                                                                                            (1-1027)
                                                                                                          US-10-618-570-2 (1-400) x AY413209
            2.37e-106
1002.50
84.6%
70.2%
48.7%
                     rercent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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/dev stage="adult"
/lab_host="E. coli SOLR"
/clone lib="Katze MMBR"
/clone="Organ: brain, Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                   organism="Macaca mulatta"
                                                                                /db_xref="taxon:9544"
/clone="IBIUW:3182"
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Location/Qualifiers
                                                 /mol_type="mRNA"
/strain="indian"
                                                                                                                   /sex="female"
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944.50
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
                                                                                                                                                                                                   708
                                                                                                                                                                                                                                                768
                                                                                                                                                                                                                                                                    ValGinGluAsnAlaPheLysGlnGlnGluGluMetArgLysLeuGluGluArg-IleTy 219
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                                                                                MetGluSerArgIleGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139
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I (bases 1 to 81)
Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
Ottenwaelder, B., Obermaier, A., Fobo, G., Han, M. and Wiemann, S.
Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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atccaagagaaaaccttcaaacaacaacaagagaaatcagtaaattagaggggcattgttaa
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Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Unpublished (2003)
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Conservative:
Mismatches:
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MEKRNTSKVEMRFTI IMEHMKDMEBRIESISNSKADLIDTERFQNFSWATDQRLANDIL
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33. .1117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; macrophage scavenger
receptor 1 (MGD)MGI:98257, GB|NM_031195, evidence: BLASIN
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                                                                                                          prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         /db_xref="FANTOM_DB:4631424C05"
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                                                                                                                                   AKO28480 13-APR-2004 MRNA linear HTC 03-APR-2004 Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631424C05 product:macrophage scavenger receptor 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3636)
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Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Mus musculus (house mouse)
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Matches:

us-10-618-570-2.rst

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US-10-618-570-2 (1-400)
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Mus musculus MSR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
                             GAACATGGGAATTCACTGGATGCAATCTCCCAAGTCCTTGCAGAGTCTGAATATGACACTG
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Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630005M03 product:macrophage scavenger receptor 1, full insert sequence.
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AK089178.1 G1:26354301
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LERRYYKUSARVOSYNKEGANHYRGESVKLANI I YNDLRLKDMEHSQTLKNI I TFI D
GPPGPQGEKGDRGLIGQTGPPGAPGIRGI PGVKGDRGQI GFPGGRGNPGAPGKPGRSG
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/db_xref="GI:26354302"
/translation="MTKEMTENQRLCPHEREDADCSSESVKFDARSMTASLPHSTKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSVQEKLKSFKAALIALYLLVFÄVLIPVVGIVTAQLLNWEMKNCLVCSRNTSDTSQGP
                                                                                                                                                                                                  /clone="F630005M03"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product; macrophage scavenger receptor 1 (MGD]MGI:98257, GB|NM_031195, evidence: BLASTN 99%, match=1461)
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                                                             organism="Mus musculus"
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/note="putative"
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                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Samamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshikayi, K., Yonada, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1509)
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
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Mus musculus (house mouse)
Mus musculus

Mus musculus

Bukaryote, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Division of Experimental Animal Research in Riken contributed to
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                    Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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DR004903 17-MAY-2005 TC109459 Human placenta, large insert, pCMV expression library Homo sapiens cDNA clone TC109459 5' similar to Homo sapiens macrophage scavenger receptor 1 (MSR1), transcript variant SR-AII, mRNA
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 768)

Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L. Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.

High-chroudphut cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
                                                                                                                                                                                                                                                                                                                                                                    PheValValLeuValProileileGlyIleValAlaAlaGlnLeuLeuLysTrpGluThr
                                                                                                                                                                                                                                                                                                                                                                                             TTTGFCGFGCTGGTGCCTATCATCGGAGTACTGGCAGCTCATCTCCTGAAATGGGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                           81 LysaanCysThrValGlySerValAsnalaAspIleSerProSerProGluGlyLysGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        578 AGTCTGAACACCACATTGCTTGATTTGCAGCTCAATGTCGAAACACTGAAAGGCAAAGTC
                                                                                                                                                                   GluserArgileGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuLeuAspAlaLysAsnPhe
                                                                                                                                                MetalaGinTrpAspAspPheProAspGinGluAspThrAspSerCysThrGluSer
                                                                                                                                                                                                                         VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro
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26
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 Matches:
Conservative:
Mismatches:
Indels:
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/clone_lib="full-length enriched swine cDNA library, adult
alveolar macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BW956649 Eull-length enriched swine cDNA library, adult alveolar macrophage Sus scrofa cDNA clone AMP010022D07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 677)
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamasima,N. and Awata,T.
PEDB (Pig EST Date Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector sequences were eliminated by RepeatMasker version 2002/07/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                              206
                                                                                                                                                                       AsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGluHisSerGlnThrLeuLysAsn 266
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of
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Animal Genome Laboratory, Genome Research Department
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Kenodai, Teukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Exar: +81-29-838-8627
Exar: +81-29-838-8627
Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped CDNA
                                                                                                                                                                                                                                            GluHisGluAsnIleIleGlyAspIleSerLysSerLeuValGlyLeuAsnThrThrVal
                              |||||||
|GAACATGGGAATTCACTGGATGCAATCTCCAAGTCCTTGCAGAGTCTGAATATGACACTG
                                                                            LeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArgValGlnGluAsnAlaPheLys
                                                                                                 GinGinGluGluMetArgiyaLeuGluGluArgileTyrAsnAlaSerAlaGluIleLys
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quality bases were trimmed based on the quality values.
Location/Qualifiers
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/tissue_type="alveolar macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BW956649 mRNA 677 bp mRNA BW956649 full-length enriched swine cDN
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/db_xref="taxon:9823"
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| arcacctrcatrcaagg 883
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Sus scrofa
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BW956649.1
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Pred. No.:
                                         999
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LOCUS DEFINITION

RESULT 11 BW956649

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

JOURNAL PUBMED COMMENT

PEATURES

REFERENCE AUTHORS

TITLE

298 100

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238

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118

178

40

120

397 140 457

337

160 517 200

637

Liu, L.,

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US-10-618-570-2 (1-400) x CB469554 (1-626)
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71.9%
35.8%
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Sus scrofa
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CB469554
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                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV6-XL4; Site 1: BcoR1; Site 2: Xhol/Sall compatible end ligatio; Oligo-d̄T primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"
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                                                                                                                                                                                                                                                                                                                                                 /clōne="TC109459"
Kiissue Lype="Placenta"
/clone_lib="Human placenta, large insert, pCMV expression
ilbrary"
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          Contact: Koves, KV,
Contact: Koves, KK
High Throughput cDNA Cloning
OriGene Technologies, Inc. (www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at OriGene Technologies, Inc.
Please contact OriGene for access.
OriGene Technologies, Inc.
Please contact Origene inc.
Fatte Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seg primer: pCNV6 Sprime forward vector primer, OriGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetAlaGlnTrpAspAspPheProAspGlnGlnGluAspThrAspSerCysThrGluSer
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32
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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 Unpublished (2005)
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Indea—Vector: pSPORTI; Site 1: NotI; Site 2: SalI; Library made from pools of polyA selected RNA, isolated at different times post-infection (0 to 16 hrs) from African swine fever virus (isolate Pretorisuskop/96/4) infected swine macrophages. Wacrophages were derived from peripheral blood mononuclear cells cultured for 48 hrs on plastic in the presence of 30% L929 supernatant."
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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                                                                                            179
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                                                                                                                                                                                       180 ValGlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArg 199
                                                                                                                                                                                                                 543 TTCCAAAATTTCAGCATGACAACTGATCAAAGATTTAATGACATTCTTCTGCAGCTAAGT
                                                                                                                       PheGlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn
                                                                                            160 SerLeuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeu
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Neilan, J.G., Kutlsh, G.F., Lu, Z., Zsak, A. and Rock, D.L.
Sequence analysis of African swine fever virus infected and
non-infected porcine macrophage cDNA libraries
Contact: Neilan JG
Contact: Neilan JG
Dlum Island Animal Disease Center
US Department of Agriculture, Agricultural Research Service
PO BOX 848, Greenport, NY 11944-848, USA
                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                626 bp mRNA linea
sn09 A05.f sn Sus scrofa cDNA 5', mRNA sequence.
CB469554
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Conservative:
Mismatches:
Indels:
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/cell_type="macrophage"
/lab_host="DH108"
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/mol_type="mRNA"
/db_xref="taxon:9823"
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/note="Vector: pCMV6-XL4; Site 1: EcoR1; Site 2: Xhol/Sall compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                            /clone="TC124536"
/tissue_type="Placenta"
/clone_lib="Human placenta, large insert, pCMV expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222
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                                                          OriGene
                                                            vector primer,
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32
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
6 Taft Ct. Suite 100
Rockville, MD 20850
http://www.origene.com
Seq primer: pCMV6 5prime forward
Technologies Inc.
                                                                                                                  sapiens"
                                                                                                     1. .651
/organism="Homo sapier
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                   Location/Qualifiers
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35.3%
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TC124536 Human placenta, large insert, pCWV expression library Homo sapiens cDNA clone TC124536 5 similar to Homo sapiens macrophage scavenger receptor 1 (MSR1), OriGene unique variant 1, mRNA
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1 (Dases 1 to 651)

Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L., Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
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                              LysAsnCysThrValGlySerValAsnAlaAspIleSerProSerProGluGlyLysGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Kovaca, Kr
High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )
Gridene Technologies, Inc. ( www.origene.com )
Tal: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at OriGene Technologies, Inc.
OriGene Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeu 196
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957 ACAGGAAAAAAAAAAGATAAGGGGAAAGACCTTAAAAAATTCCCAATGATCTCAAAATG 1016
                                                                                                          nMetGluSerArgIleGlnTyrLeuSer-AspAsnGluAlaAsnLeuLeuAspAlaLysA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 GluGluIleLygGlyGluMetLygLeuLeuAsnAsnIleThrAsnAspLeuArgLeu 255
                                                            357 TCCCTTCAAGAGAAACTGAAGTCCTTCAAAGCTGCACTGATTGCCCTTTACCTTCTTT
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                                                                                                      CN643736

LLUMIGEN MCO 8498 Katze MMBR Macaca mulatta cDNA clone IBIUW:3182
5' similar to Bases 116 to 1087 highly similar to human MSR1

HE 436887), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
/lab_host="E. coli SOLR"
/clome lib="Xctze MMBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site_1: BcoR I;
Site_2: Xho I; Created from Stratagene ZAP-cDNA Synthesis kit [catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (Catalog #200450)"
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.

I (bases I to 1093)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. ar Iadonato, S.P.
                                                                                                                                                                                                                                                                                                                                                                                        Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human Genome Blol. 6 (7), R60 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: C. Magness
11luwigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
7El: 2063780400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.01.15. 487 Q20 bases.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 1093 Std Brror: 0.00
Plate: CL000089 row: C column: 03
Seg primer: CCCTCACTAAAGGGAACAAA
POLYA=Yee.
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/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:9544"
clone="IBIUW:3182"
                                                                                                                                                                                                                                    Macaca mulatta (rhesus monkey)
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CN643736.1 GI:47154746
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200 ValGinGlu 202
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643 ATCCAAGAG 651
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AUTHORS
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1 MetAlaGinTrpAspAspPheProAspGinGluAspThrAspSerCysThrGluSer

US-10-618-570-2 (1-400) x CN643736 (1-1093)

1093 162 44 64 10

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

4.4e-73 719.50 73.6% 57.9% 34.9%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

Pred. No.:

ValLysPheAspAlaArgSerValThrAlaLeu-LeuProProHisProLysAsnGlyPr 40

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776

(Oldsn) XWAJE JOKE SIMI

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Add 7731 Human Bca
Aat 2265 Human DNA
Aat 43260 Type II m
Aca5662 Human DNA
Add 56458 Human Dol
Add 15458 Human DNA
Add 15259 Type I ma
Adt 259164 Human DNA
Add 38907 Human SNP
Add 38907 Human SNP
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1071. 2269
14189= a /
/product= "ScR/avidin fusion protein"
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ADV78151
AAZ49865
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ADP24728
AAT68796
AAQ28539
ADG39681
ADG39730
ADP86098
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ADQ38904
AAS94868
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ADQ38907
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AAQ47730
AAT43259
AAF29164
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-Q=Abss/ABSSMBs spool/V310618570/runat_27022006_063853_13038/app_query.fasta_1
-Q=Abss/ABSSMBs spool/V310618570/runat_27022006_063853_13038/app_query.fasta_1
-DB=N Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LGOPCL=0 -LGOPEXT=0
-UNITS_bits -START=1 -END=-1 -MATRIX.Fallosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UOTFWM=pto -NORM=ext -HEAPSIZES=500 -MINIEN=0 -MAXIEN=2000000000 -HOST=abss05p
-USER=USI0618570_@CGN 1 1 1096_@runat_27022006_063853_13038 -NCPU=6 -ICPU=3
-NO WMAP -NEG_SCORES=0 -WAIT -DSPBADCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELUEXT=7
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Aag04926 Sequence
Aag28540 DNA for b
Aag04925 Sequence
                                                                                             February 27, 2006, 08:46:22; Search time 646 Seconds (without alignments) 4126.745 Million cell updates/sec
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                                                                    - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence encoding portion of scavenger receptor protein with affinity acylated low density lipoprotein (aLDL).
                                                                                              GGGGAAATGAAACTGTTGAATAATAATCACTAATGATGAGGCTGAAGGATTGGGAACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyLysGluValLeuLysThrMetTrpLeuLeuArgSerSerValAsnAspIleGlyAsp
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                                                                             GlnGluAenAlaPheLyeGlnGlnGluGluMetArgLysLeuGluGluArglleTyrAen
                                                                                                                                            221 AlaSerAlaGluIleLysSerLeuAspGluLysGlnValTyrLeuGluGlnGluIleLys
                                                                                                                                                              GCATCAGCAGAAATTAAGTCTCTAGATGAAAAACAAGTATATTTGGAACAGGAAATAAAA
                                                                                                                                                                                                         GlyGluMetLysLeuLeuAsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGluHis
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                GlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArgVal
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                                                                                                                                                                                                                                                  This invention describes a novel protein (A) which comprises a membrane-spanning domain and an extracellular domain (BCD), where the ECD comprises biotin-binding activity. Using the proteins or encoding nucleic acid molecules it is possible to target biotinylated molecules to specific sites in tissues. Molecules targeted in this way may be taken up by the tissues or cells by endocytosis, allowing the molecules to exert their effects within or on the cell. This sequence encodes a bovine scavenger receptor class Alavidin fusion protein which is used in the description of the invention
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                                                                                                                                                         New fusion proteins having an extracellular domain with biotin-binding activity, used to target biotinylated molecules to specific sites in
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                                                            604 CAAGAGAATGCATTTAAACAACAAGAGGAGATGCGTAAATTAGAGGAGCGTATATACAAT
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Labelled Abs, raised to the protein may be injected into the vascular system to detect the presence of atherosclerotic plaques. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR 2003 to co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGAAGTICGAIGCTCGCTCAGTGACAGCTTTGCTTCCTCCCCATCCTAAAAATGGCCCA 123
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                                                                                                                                                                             New receptor protein - has affinity for acetylated low density
lipoprotein and corresponding antibodies and DNA sequences.
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                                     (MASI ) MASSACHUSETTS INST TECHNOLOGY
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                                                                                                                              The bovine scavanger receptor protein gene was isolated by screening a bovine lung cDNA library with degenerate probes designed based on fragments of the purified accavanger receptor protein. The DNA encodes a scavanger receptor protein. The DNA encodes a scavanger receptor protein. The DNA encodes a scavanger receptor protein of the scavanger receptor protein inactivate extracellular portion of the scavanger receptor protein inactivate endotoxin-related substances and are used in the diagnosis and treatment of endotoxaemia. They may be administered to patients at high risk of symptomatic or endotoxic shock. The fragments may also be fixed to inert supports for purificin. purposes. The fragments may also be fixed to inert greater binding affinity for the endotoxin-related substance than the native scavanger receptor protein, or to more effectively neutralise the toxic or pathogenic effects of mole. That bind the scavanger receptor protein or of organisms which express such mols. See also AAQ28536-9.
                                                            Treatment and diagnosis of endotoxaemia and related disease states -
using a polypeptide fragment of the extracellular portion of a macrophage
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                                                                                                            Disclosure; Page 36; 56pp; English
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1381.50
79.4%
73.6%
67.1%
                                                                                       scavenger receptor protein.
                                     WPI; 1992-315935/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             844 GGAGATAGAGGCCC-TCCTGGACA---AAATGGTATACCAGGCTTTCCAGGTCTAATAGG
                                                                                                                                                                                       GinGluAsnAlaPheLysGlnGlnGluGluMetArgLysLeuGluGluArgIleTyrAsn
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TTACTTTCCTCCATCCAGGAACATGAGAATATCATAGGGGATATCTCCAAGTCATTAGTA
                                                             GlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArgVal
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                                                                                  GGTCTGAACACCACAGTACTTGATTTGCAGTTCAGTATTGAAACACTGAATGGCAGAGTC
                                                      GlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArgVal
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reduced immunogenicity; trimerisation; CD40L; immune response;
T-cell activation; isotype switching; gene.
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/product= "Macrophage scavenger receptor"
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P-PSDB; ADB89003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor protein, and fragments and analogues thereof may be imobilised on a support and used in assay and purification of the aLDL target. Labelled Abs. raised to the protein may be injected into the vascular system to detect the presence of anceleroic plaques. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 ACTCTTCAAGAGAGGATGAAGTCTTATAAAACTGCACTGATCACCCTTTATCTCATTGTG 215
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                                                                                                                                                                                                                                                                                                                                                                      New receptor protein - has affinity for acetylated low density lipoprotein and corresponding antibodies and DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1807 BP; 556 A; 384 C; 406 G; 461 T; 0 U; 0 Other;
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89US-00391486.
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New fusion polypeptide that is capable of forming a trimer, useful in preparing a composition for treating immune related or inflammatory disorders.
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4; 24pp; English Example, Fig

The present invention relates to a polypeptide comprising a fusion protein capable of forming a trimer and comprising a heptad repeat containing region of the human macrophage scavenging factor protein containing region of the human macrophage scavenging factor protein appearing as ADB89007 fused to a second protein (specially a member of the tumour necrosis superfamily, TNFSF e.g. CD40L). CD40L is involved in sotype switching and is important in T-cell activation in the immune seponse. The fusion protein has reduced immunogenicity due to its ability to form trimers. Also included are the nucleic acids encoding the fusion proteins and a recombinant vector comprising the nucleic acid. The fusion proteins are used to deliver a therapeutic protein with reduced immunogenicity to a patient in need of the protein. The present sequence encodes the human macrophage scavenaging factor protein. Note:

The authors have mixed up the descriptions of the sequences as they appear in the figures, therefore there is a possibility that the

Sequence 1077 BP; 364 A; 221 C; 242 G; 250 T; 0 U; 0 Other;

61 GTGAAATTTGATGCTCGCTCAATGACAGCTTTGCTTCCTCCGAATCCTAAAAACAGCCCT 120 ||||||||||:::||| | AAGAATTGCTCAGTTAGTTCAACTAATGCAAATGATATAACTCAAAGTCTCACGGGAAAA 300 PheglnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn 159 SerLeuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeu 179 GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn 119 MetGluSerArglleGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139 481 ACCTIGITITICCTCAGICCAGGGACAIGGGAAIGCAAIAGAIGAAAICTCCAAGICCTIA 540 180 ValGlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArg 199 VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro 40 PheValValLeuValProlleileGlyIleValAlaAlaGlnLeuLeuLysTrpGluThr 80 LysAsnCysThrValGlySerValAsnAla---AspileSerProSerProGluGlyLys 99 MetAlaGlnTrpAspAspAspPeProAspGlnGlnGluAspThrAspSerCysThrGluSer ThrLeuGlnGluArgMetLysSerTyrLysThrAlaLeuIleThrLeuTyrLeuIleVal 1077 197 41 34 1 Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The gene can be expressed from a cytomegalovirus promoter in a host cell eg. CHO cell. The resulting recombinant scavenger receptor can be used to detect modified lipoproteins or modified substances in the blood. See also AAQ21549. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                    LysGlyGluMetLysLeuLeuAsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGlu
220 AsnAlaSerAlaGluIleLysSerLeuAspGluLysGlnValTyrLeuGluGlnGluIle
                                                                                                                                   721 AAAGGAGAAGTGAAAGTACTGAATAACATCACTAATGATCTCAGACTGAAAGATTGGGAA
                             200 ValGinGluAsnAlaPheLysGlnGlnGluGluMetArgLysLeuGluGluArglleTyr
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               347 GGAAATGACAGCGAAGGAAATGAGATTTCAAGAAGTCTTTATGGAACACATGAGCAAC
                                                                                                                                                                                                                            AAAGGAGAAGTAGAAAGTACTGAATAACATCACTAATGATCTCAGACTGAAAGATTGGGAA
                                                VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro
                                                         GTGAAATTTGATGCTCGCTCAATGACAGCTTTGCTTCCTCCGAATCCTAAAAAACGGCCCT
                                                                               ThrieuGinGluArgMetLysSerTyrLysThrAlaLeuIleThrLeuTyrLeuIleVal
                                                                                         PheValvalLeuValProIleIleGlyIleValAlaAlaGlnLeuLeuLygTrpGluThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in AAQ47730-31 encode the human scavenger receptors I and II. The proteins encoded by these sequences may be used in the production of antihuman scavenger receptor antibodies (AHSRA). These peptides were used to immunise a mammal, pref. a rabbit, and anti- serum was prepared. A monoclonal antibody was prepared from HAP- resistant hybridoma. These antibodies may be used to determine the progress of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 progress
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| AAGAATTGCTCAGTTAGTTCAACTAATGCAAATGATATAAACTCCAAAGTCTCACGGGAAAA
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Location/Qualifiers 47. .1123
                                                                                                                                            "HSR-II"
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MetGluSerArg1leGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139
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                                                                          MetAlaGlnTrpAspAspPheProAspGlnGlnGluAspThrAspSerCysThrGluSer
                                                                                                                                  21 VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro
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ATAAGTTTGAATACCACATTGCTTGATTTGCAGCTCAACATAGAAAATCTGAATGGCAAA
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cell substrate; cell attachment; atherosclerosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-human scavenger receptor antibody useful for the identification the determination of macrophages.
                                                          SerLeuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeu
                                                                                                    ValGlyLeuAsnThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArg
                                                                                                                                                           ValGlnGluAsnAlaPheLysGlnGlnGluMetArgLysLeuGluGluArglleTyr
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                                                                                                                                                                                                                                                                              LysGlyGluMetLysLeuLeuAsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGlu
                                                                                                                                                                                                                                                                                             Human; type II scavenger receptor; antibody; macrophage; ds
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                                                                                                                                                                                                                                                                        Human type I and type II macrophage scavenger receptor genes (AAT43259 and AAT43260, respectively) can be used to transfect human embryonic kidney 293 cells. The transfected cells show an enhanced ability to attach to a solid support and are useful for screening cpds. for biological activity, or for identifying antagonists of the scavenger receptor gene, e.g. to develop agents for treatment of atherosclerosis
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                                                                                                                                                                                                               New modified human embryonic kidney 293 cells - transfected with a mammalian scavenger receptor gene to enhance ability to attach to a
                                                                                                                                                                                                                                                                                                                                          Sequence 1367 BP; 427 A; 298 C; 303 G; 339 T; 0 U; 0 Other;
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                           Location/Qualifiers
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          sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; probe; as; array element; Parkinson's disease;
signalling pathway population; cancer; adenocarcinoma; leukaemia;
immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
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ATAAGTTTGAATACCACATTGCTTGATTTGCAGCTCAACATAGAAAATCTGAATGGCAAA
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PheGlnAsnPheSerlleThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn
                                   SerLeuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeu
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discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoms and leukaemia, immunopathies e.g. AlDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide form part of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic
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The invention relates to a composition of polymucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polymucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polymucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Composition and laso be used for monitoring the progression of diseases that may be associated with the altered expression of diseases that may be associated with the altered expression of diseases that may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. dementia, ammesta, a meast for cultiple plands, bladder, bear appression. This sequence represents a cepilepsy, Allaheimer's diseases or depression. This sequence data for human polynucleotide probe of the invention. Note: The sequence data for
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      AAAGGAGAAGTGAAAGTACTGAATAACATCACTAATGATCTCAGACTGAAAGATTGGGAA
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this patent did not form part of the printed specification obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
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The gene can be expressed from a cytomegalovirus promoter in a host cell e.g. CHO cell. The resulting recombinant scavenger receptor can be used to detect modified lipoproteins or modified substances in the blood. See also AAQ21550. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New scavenger receptor-producing animal cells - which have been transformed with vector contg. gene for coding human scavenger receptor or II type under control of promoter, etc.
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                                                                                                                                                                                                                                                                                                                              /*tag= a
/product= "scavenger_receptor_type_I"
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                  Location/Qualifiers 47. .1402
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BP.
DNA; 2028
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                                                                                      (revised)
(first entry)
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P-PSDB; AAR21512.
standard;
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                                              The sequences given in AAQ47730-31 encode the human scavenger receptors I and II. The proteins encoded by these sequences may be used in the production of antihuman scavenger receptor antibodies (AHSRA). These peptides were used to immunise a mammal, pref. a rabbit, and anti- serum was prepared. A monoclonal antibody was prepared from HAT- resistant
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Matches:
Conservative:
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                          Page 5-7; 10pp; Japanese.
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arteriosclerosis
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                          Claim 2;
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                                                                             MetGluSerArglleGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139
                                                                                             AsnAlaSerAlaGluIleLysSerLeuAspGluLysGlnValTyrLeuGluGluIle 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, scavenger receptor, antihuman scavenger receptor antibody; AHSRA;
mammal; rabbit; antiserum; monoclonal; HAT-resistant hybridoma;
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                                         TTCCAAAATTTCAGCATGACAACTGATCAAAGATTTAATGACATTCTTCTGCAGCTAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                       227 TTTGCAGTTCTCATCCCTCTCATTGGAATAGTGGCAGCTCAACTCCTGAAGTGGGAAACG
                                                                                                                                      81 LysAsnCysThrValGlySerValAsnAla---AspIleSerProSerProGluGlyLys
                                                                                                                                                         ValGlnGluAsnAlaPheLysGlnGlnGluGluMetArgLysLeuGluGluArglleTyr
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                                                                              PheValValLeuValProIleIleGlyIleValAlaAlaGlnLeuLeuLysTrpGluThr
                     ThrieuGlnGluArgMetLysSerTyrLysThrAlaLeuIleThrLeuTyrLeuIleVal
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16-AUG-1991;
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New modified human embryonic kidney 293 cells – transfected with a
mammalian scavenger receptor gene to enhance ability to attach to a solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIGAAATTIGAIGCICGCICAAIGACAGCIITGCIICCICCGAATCCIAAAAACAGCCCI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Met. AlaGinTrpAspAspPheProAspGinGinGluAspThrAspSerCysThrGluSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human type I and type II macrophage scavenger receptor genes (AAT43259 and AAT43260, respectively) can be used to transfect human embryonic kidney 293 cells. The transfected cells show an enhanced ability to attach to a solid support and are useful for screening cpds. for biological activity, or for identifying antagonists of the scavenger receptor gene, e.g. to develop agents for treatment of atherosclerosis
                                                                                                                                                                                                                                                       I macrophage scavenger receptor; SRG; kidney; 293 cell; substrate; cell attachment; atherosclerosis; ds.
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                                            HisserGlnThrLeuLysasnlleThrLeuLeuGlnGly 272
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                                                                                                                                     AAT43259 standard; cDNA to mRNA; 2028
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47. .1402
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P-PSDB; AAW08077.
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                                                                                              human type I or type II scavenger receptor epitope. The anti-scavenger receptor antibody can be used for the identification and determination of macrophages. The present sequence represents DNA encoding the human type I scavenger receptor
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                                    anti-human scavenger receptor antibody useful for the identification the determination of macrophages.
                                                                                      This invention relates to a poly or monoclonoal antibody which targets a
                                                                                                                                                                                                                                                             PheValValLeuValProIleIleGlyIleValAlaAlaGlnLeuLeuLygTrpGluThr
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Matches:
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Search completed: February 27, 2006, 09:40:04 Job time : 659 secs Sequence 6, Appli Sequence 2, Appli Sequence 3, Appli Sequence 57, Appl Sequence 18, Appl Sequence 11721, A Sequence 13815, A

Sequence 13834, 7 Sequence 13844, 7 Sequence 13854, 7 Sequence 13814, 7 Sequence 13813, 7

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Sequence 13832, P. Sequence 13842, P. Sequence 13850, P. Sequence 1, Appl. Sequence 3, Appl. Sequence 3, Appl.

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Sequence 13811, Sequence 13820, Sequence 13829,

Sequence 3, Appl seguence 13838, sequence 13849

Sequence 123, App Sequence 569, App Sequence 56, App Sequence 41, Appl Sequence 41, Appl Sequence 1, Appli

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INFORMATION: Recombinant cDNA encoding fusion protein
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APPLICANT: Kulomaa, Markku
APPLICANT: Lehtolainen, Pauliina
APPLICANT: Lehtolainen, Pauliina
APPLICANT: Airenne, Kari
TITLE OF INVENTION: Bitcin-Binding Receptor Molecules
FILE REPERBECE: GJE-48
CURRENT APPLICATION NUMBER: US/10/618,570
CURRENT APPLICATION NUMBER: US/10/618,570
FILE REPERBECE: GJE-48
PRIOR PILING DATE: 2002-07-11
PRIOR PILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH. 5177
                                                                                                                                                    US-10-724-527-3
US-10-891-576-57
US-10-891-576-57
US-10-891-576-57
US-10-741-600-13815-
US-10-741-600-13834
US-10-741-600-13854
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US-11-093-776-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10618570 Publication No. US20040185059A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1071)..(2270)
; OTHER INFORMATION:
US-10-618-570-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAMB/KEY: CDS
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-DB=Published Applications NA Main -QFWT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
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Sequence 1, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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2: /cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO8 PUBCOMB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-305-720-1260

US-10-426-262-1

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Maximum Match 1008
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Score

Result

Qy 321 LeutisGlyThrGlnAsnThrIleAsnLysArgThrGlnProThrPheGlyPheThrVal 340 Db 2031 CTGCATGGGACACAAACACCATCAACAAGAGGACCCAGCCCACCTTTGGCTTCACCGTC 2090 Qy 341 AsnTrpLysPheSerGluSerThrThrValPheThrGlyGlnCysPheIleAspArgAsn 360 Db 2091 AATTGGAAGTTTTCAGAGTCCACCACTGCTTCACAGGACTTCATAGACAGGAAT 2150 Qy 361 GlyLysGluValLeuLysThrMetTrpLeuLeuArgSerSerValAsnAspIleGlyAsp 380 Db 2151 GGGAAGGACCTGAAGACCATGTGCTTCAGGGCCAGTGCTTCATAGACATTGGTGAT 2210 Qy 381 AspTrpLysAlaThrArgValGlyIleAsnIlePheThrArgLeuArgThrGlnLysGlu 400 Db 2211 GACTGGAAAGCTGCGGCATCAACATCACTGCCTGCCTGCGCACAGGAAGAAG 2270	RESULT 2 US-10-326-186-5 Sequence 5, Application US/10326186 Publication No. US20033119149A1 GENERAL INFORMATION: TITLE OF INVENTION: Timeric Recombinant Polypeptides FILE REPERENCE: 3398-A CURRENT APPLICATION NUMBER: US/10/326,186 CURRENT PILING DATE: 2002-12-20 NUMBER OF SEQ ID NOS: 10 SOCTWARE: Patentin version 3.1 SEQ ID NO 5 LENGTH: 1077 FYPE: DNA PRATURE: NAME/KEY: CDS LOCATION: (1)(1077) OTHER INFORMATION:	ignment Scores: 6.01e-94	Tricturing that greet, years are the state of the state o
ed. No.: 1.34e-194 Matches: 5177 2059.00 Matches: 400 conservative: 100.04 Mismatches: 0 ery Match: 100.04 Mismatches: 0 Gaps: 0 -10-618-570-2 (1-400) x US-10-618-570-1 (1-5177) 1071 ATGCACAGTGGGATGACTTTCCTGATCAGCAAGAGGACACTGAAGGTCT 21 ValLy8PheAspAlaArgSerValThrAlaLeuLeuProProHisProLy8AsnGlyPro	131 GTGAAGTTCGATGCTCGGTGACAGTTTGCTTCCTCCCCATCCTAAAAATGGCCCA 1190 1131 GTGAAGTTCGATGCTCGGTGACGTTTTGCTTCCTCCCCATCCTAAAAATGCCATCGTGATCACCCTTATCATGTG 1250 1191 ACTCTTCAAGAGACATGAAGTCTTATAAAACTGCACTGATCACCCTTATCTCATTGTG 1250 1191 ACTCTTCAAGAGAGATGAAGTCTTATAAAACTGCACTGATCACCCTTATCTCATTGTG 1250 1191 ACTCTTCAAGAGAGCATGGCTTGACTCACTCAGACTCACCCTTATCATTGTG 1250 1191 ACTCTTCATGCCCATCATTGGCATAGAGAGATCAGACTCAGAATGGAAAACG 1310 1191 AAAAACTATCAAGATTAAAAAAAAAAAAAAAAAAAAAAA	Oy 141 GlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsnSer 160 1491 CAAATTTCAGCATAACATGATCAAAGATTTAATGATCTTTTCCACTAAATTCC 1550 Oy 161 LeuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLySerLeuVal 180 1551 TTACTTTCCTCCATCCAGGAAATTACATGAGGGGATATCTCCAAGTCATTAGTA 1610 Oy 181 GlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArgVal 200 161 GlyLeuAsnThrThrValLeuAspLeuGlnDheSerIleGluThrLeuAsnGlyArgVal 200 161 GlnGluAsnAlaPheLysGlnGluGluGluAetaTGAAAGGGGAAATGAAAGGCAAGTC 1670 Oy 201 GlnGluAsnAlaPheLysGlnGluGluGluAetagLysLeuGluGluArgIleTyAsn 220 1671 CAAGAGAATGCATTTAAACAAGAGGAGGATGCTAAATTAGAGGGAGG	Qy 241 GlyGluMetLysLeuLeuAsnasnileThrAsnAspLeuArgLeuLysAspTrpGluHis Db 1791 GGGGAAATGAACTGTTGAATAATCACTAATGATCTGAGGTTGAGGAATTGGGAACAT 1850 Qy 261 SerGlnThrLeuLysAsnIleThrLeuLeuGlnGlyAlaargLysCysSerLeuThrGly 280 Db 1851 TCTCGAGATTGAAAAATTACCTCTAAGGTGCCAGAAATGCTCTACTGGG 1910 Qy 281 LysTrpThrAsnAspLeuGlySerAsnMetThrIleGlyAlavalaAlavalAsnSerArgGlyGlu 300 Db 1911 AAATGGACCACACACTCGACTCGACCACCACCTGGGGGCTGTGAACAGCAGGGGGTGAA 1970 Qy 301 PheThrGlyThrTytleThrAlaValThrAlaThrSerAsnGluIleLysGluSerPro 320 PheThrGlyThrTytlleThrAlaValThrAlaThrSerAsnGGAGGTGAA 1971 TTCACAGGCACCTACACACACACACACACACACACACACA

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APPLICANT: Xu, Jianfeng.
APPLICANT: Xu, Jianfeng.
APPLICANT: Meyers, Deborah
APPLICANT: Shang, Sigun
APPLICANT: Walsh, Patrick C.
APPLICANT: Isaacs, William B.
APPLICANT: Bleecker, Eugene
TITLE OF INVENTION: MYTATIONS IN THE MACROPHAGE SCAVENGER RECEPTOR 1 GENE ALTER RISK
TITLE OF INVENTION: OF PROSTATE CANCER, ASTHWA, AND CARDIOVASCULAR DISEASE
FILE REPERENCE: 9151-23
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CURRENT FILING DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 2
SOCTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 2028
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; Publication No. US20040018521A1
; GENERAL INFORMATION:
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OTHER INFORMATION: Genbank ID No. US20040010136A1 g219991
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                                       US-10-618-570-2 (1-400) x US-10-426-262-1 (1-2028)
                              Gaps:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES:
FILLE REPERENCE: CLORO1499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 570
LENGTH: 2877
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-600-570
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                                                                                                                                                                                                                                                               Sequence 567, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, MICHELE et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND UPTION OF TITLE REPRENCE: CLOOH499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FESTESEQ for Windows Version 4.0
SEQ ID NO 567
LENGTH: 3525
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ORGANISM: Homo sapiens
US-10-741-600-567
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                                                                                                                                        APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001499
CURRENT FILING DATE: 2003-12-22
CURRENT FILING DATE: 2003-12-22
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 568
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                                                                                                     Sequence 568, Application US/10741600 Publication No. US20050026169A1 GENERAL INFORMATION:
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ATGGAGAAGAGAATCCAGCATATTTAGACATGGAAGCCAACCTCATGGACACAGAGCAT 579
                                                                                                                                   SerleuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeu
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APPLICANT: SHIFFMAN, Dov
APPLICANT: SOMOGYI, Roland
APPLICANT: SOMOGYI, Roland
APPLICANT: SELLAMER, Jeffney J.
APPLICANT: ARECARD M.
APPLICANT: APPLICANT: ARECARD M.
APPLICANT: APPLICANT: ALAW, RICHARD M.
APPLICANT: TAI, Julie
APPLICANT: TAI, Julie
APPLICANT: APPLICANT: ALI, Julie
CURRENT APPLICANT: APPLICA
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OTHER INFORMATION: Incyte ID No. US20030165924A1 344240.
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Matches:
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Publication No. US20030165924A1
GENERAL INFORMATION:
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| NAME/KEY: ungure
| LOCATION: 3522, 3634-3635, 3699
| OTHER INFORMATION: a, t, c, g, or
| US-10-240-965-123
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Best Local Similarity:
Query Match:
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US-10-240-965-123
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Pred. No.:
Score:
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Sequence 569, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE REPRESENCE: CLOR01499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 569
LENGTH: 3719
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                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                              Gaps:
                   3.56e-93
1042.50
87.2%
72.2%
50.6%
; ORGANISM: Homo sapiens
US-10-741-600-569
                        Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                        US-10-618-570-2 (1-400)
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US-10-741-600-566
              Alignment Scores:
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Sequence 566, Application US/10741600 Publication No. US20050026169A1

THEREOF 119 219 279 339 459 519 579 639 SerieuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSeriysSerieu 179 669 399 MetGluSerArgileGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139 PheGlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn 159 ValGlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArg 199 219 239 819 879 40 9 80 66 GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES:
FILE REPREBNCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SSOFTWARE: PSELSEQ for Windows Version 4.0
LENGTH: 3791 20 ValGinGluAsnAlaPheLysGlnGlnGluGluMetArgLysLysLeuGluGluArgIleTyr MetalaGinTrpAspAspPheProAspGinGinGluAspThrAspSerCysThrGluSer PheValValLeuValProIleIleGlyIleValAlaAlaGlnLeuLeuLygTrpGluThr LyshanCysThrValGlySerValAsnAla---AspIleSerProSerProGluGlyLys GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn TTCCAAAATTTCAGCATGACAACTGATCAAAGATTTAATGACATTCTTCTGCAGCTAAGT 3791 197 41 34 1 Length:
Matches:
Conservative:
Mismatches:
Indels: x US-10-741-600-566 (1-3791) 3.66e-93 1042.50 87.2% 72.2% 50.6% TYPE: DNA CORGANISM: Homo sapiens US-10-741-600-566 Percent Similarity: Best Local Similarity: Query Match: DB: US-10-618-570-2 (1-400) 220 ò 셤

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180 ValGlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArg 199
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                                                              200 ValGinGluAsnAlaPheLysGlnGlnGluGluMetArgLysLeuGluGluArgileTyr
                                                                             661 AATGCATCAGCAGAAATTATGTCTATGAAAGAAGAAGAACAAGGAACAGAAATA
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| Publication No. US20030186303A1
| GENERAL INFORMATION:
| APPLICATION No. US2003018630A1
| APPLICATION TIXIN
| TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS
| FILLE REFERENCE: CDS 266 US NP
| CURRENT PELICATION NUMBER: US/10/394,382
| CURRENT FILING DATE: 2003-03-21
| PRIOR PLING DATE: 2002-03-29
| NUMBER OF SEQ ID NOS: 49
| SOFTWARE: PATENTION OF 13.1
| SEQ ID NO 41
| LENGTH: 1330
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Matches:
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CRGANISM: human
US-10-394-382-41
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Pred. No.:
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US-10-394-382-41
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LysGlyGluMetLysLeuLeuAsnAsnAsnAsnAspLeuArgLeuLysAspTrpGlu 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetGluSerArgIleGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheGlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLeuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeu 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCGCAGTGGGACAGCTTCACTGATCAACAGGAGGACACTGATAGCTGTTCAGAATCT
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                                                                                                                                                                                                                                                                                                                                                                   1330
189
44
139
                                                 ; Sequence 41, Application US/10393892; Publication No. US20030186302A1; Publication No. US20030186302A1; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: COLORECTAL CANCER DIAGNOSTICS; FILE REFERENCE: CDS 267 US NP; CURRENT APPLICATION NUMBER: US/10/393,892; CURRENT FILING DATE: 2003-03-21; PRIOR FILING DATE: 2002-03-29; NUMBER OF SEQ ID NOS: 49
; SOFWARE: Patentin version 3.1
; SEQ ID NO 41; LEUTH: 1330
                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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85.3%
69.2%
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: human
US-10-393-892-41
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Pred. No.:
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US-10-393-892-41
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                                                                                                                                  ThrThrValPheThrGlyGlnCysPheIleAspArgAsnGlyLysGluValLeuLysThr
                                                                                                                                                                                                                                                                                                                                                            368 MetTrpLeuLeuArgSerSerValAsnAspIleGlyAspAspTrpLysAlaThrArgVal
                                                                                                                                                                                                                                                                                                                                                                                             358 ATGTGGCTCCTGAGGAGCTCCGTGAATGACATCGGCGACGACGACTGGAAGGCCACCCGCGTG
                                                                                                                                                                                                                                                                                                        298 ACCACCGTGTTCACCGGCCAGTGCTTCATCGACCGCAACGCCAAGGAGGTGCTCAAGACC
                                                                                                          AlaValThrAlaThrSerAsnGluIleLysGluSerProLeuHisGlyThrGlnAsnThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-US--/16-6

Sequence 6. Application US/11093776

Publication No. US2005017236A1

Publication No. US2005017236A1

Publication No. US2005017236A1

Publication No. US2005017236A1

APPLICANT: Christeller, John Tane

APPLICANT: Marray, Colleen

APPLICANT: Marray, Colleen

APPLICANT: Malone, Louise Anne

APPLICANT: Philip, Bruce Alna

APPLICANT: Phing, Malone, Louise Anne

APPLICANT: Phung, Thai Hong

APPLICANT: The Horticulture and Food Research Institute of

APPLICANT: The Malone, Louise Anne

APPLICANT: The Marray Phung, Thai Hong

APPLICANT: The Marray Phung, Margaret Mary

APPLICANT: New Zealand Limited

TITLE OF INVENTION: Planeric Polypeptides Allowing Expression of

TITLE OF INVENTION: Planeric Polypeptides Allowing Expression of

FILE REFERENCE: 020829-00010008

CURRENT FILING DATE: 2008-03-29

PRIOR PILING DATE: 2001-01-12

PRIOR FILING DATE: 1998-07-15

PRIOR PAPLICATION NUMBER: WO PCT/N299/00110

PRIOR FILING DATE: 1999-07-15
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Matches:
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OTHER INFORMATION: PPI-I/Avidin fusion protein
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 486
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Percent Similarity:
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Query Match:
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NAME/KEY: CDS
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JEDENARY: BOOTLAND: LINDA M.
JAPPLICANT: BELFUSS, KATHERINE
JAPPLICANT: BILKA, JOSEPH
JAPPLICANT: LIZAMA, JOSEPH
JAPPLICANT: LIZAMA, JOSEPH
JAPPLICANT: LIZAMA, JOSEPH
JAPPLICANT: LIZAMA: BARRY
JITLE OF INVENTION: IMMUNIZATION OF FISH WITH PLANT-EXPRESSED RECOMBINANT
JITLE OF INVENTION: PROTEINS
JITLE OF INVENTION NUMBER: 60/433,381
PRIOR FILING DATE: 2002-12-13
JUMBER: OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver: 3.2
SEQ ID NO 1
LENGTH: 459
                                                                                                                          PheGlnAsnPheSerlleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn 159
                                                                                                                                                                                                                                    180 ValGlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArg 199
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                                         MetGluSerArgileGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139
                                                                     421 TTTCAAAATTTCAGTGTGACAACTGATCAACGATTTGCTGATGTTCTTCTCCAACTAAGT 480
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Matches:
Conservative:
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Publication No. US20040175441A1
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ORGANISM: Hordeum vulgare
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US-11-US-2/2-1-US-2/2

Sequence 2, Application US/11093776

Publication No. US20050172356A1

GENERAL INFORMATION:

APPLICANT: Sutherland, Paul William
APPLICANT: Markwick, Ngaire Patricia

APPLICANT: Markwick, Ngaire Patricia

APPLICANT: Philip, Burce Allan

APPLICANT: Philip

APPLICANT: Philip

APPLICANT AND APPLIC
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OKGANIDN: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:avidin cDNA
OTHER INFORMATION: (pGEMav)
FEATURE:
NAME/KEY: CDS
OTHER INFORMATION: (44)...(502)
OTHER INFORMATION: avidin (pGEMav)
FEATURE:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                               US-10-618-570-2 (1-400) x US-11-093-776-2 (1-576)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: February 27, 2006, 10:42:01
he : 1037 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTCGCCTGCGCACACAGAAGGAG 499
; NAME/KEY: sig_peptide
; LOCATION: (44)..(115)
; OTHER INFORMATION: signal sequence
US-11-093-776-2
                                                                                   6.8e-58
678.00
100.0%
100.0%
32.9%
                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                          Alignment Scores
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393
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OM protein

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Run

Sequence:

Title:

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Sequence 13114, A Sequence 13114, A Sequence 13114, A Sequence 10016, A Sequence 10006, A Sequence 10006, A Sequence 10006, A Sequence 10001, A Sequence 10010, A Sequence 10011, A Sequence 10018, A Sequence 10018, A Sequence 10018, A Sequence 10018, A Sequence 10029, A Sequence 10039, A Sequence 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 372, 74plication US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION:
TITLE OF INV
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   US-10-995-561-368
US-10-995-561-1314
US-10-995-561-1314
US-10-995-561-10014
US-10-995-561-10016
US-10-995-561-10016
US-10-995-561-10016
US-10-995-561-10019
US-10-995-561-10029
US-10-995-561-10029
US-10-995-561-10029
US-10-995-561-10029
US-11-128-049-1104
US-11-128-049-1104
US-11-128-049-1106
US-10-995-561-10069
US-10-995-561-10069
US-10-995-561-10069
US-10-995-561-10069
US-10-995-561-10069
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Matches:
Conservative:
Mismatches:
Indels:
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; ORGANISM: HOMO
US-10-995-561-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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         Score:
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-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
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(without alignments)
1682.341 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 372, 1
Sequence 370, 1
Sequence 369, 1
Sequence 371, 1
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1: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                                    GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                   nucleic search, using frame_plus_p2n model
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US-10-995-561-370
US-10-995-561-369
US-10-995-561-371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
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                                                                                                                                                                                                            February 27, 2006, 09:29:22
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum Match 100%
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length: 2000000000
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Database

Š. Result

Minimum DB Maximum DB

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; LENGTH: 3336
; TYPE: DNA
; ORGANISM: HOMO 8
US-10-995-561-370
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US-10-995-561-369
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                              ||||||||||:::|||
| AAGAATTGCTCAGTTAGTTCAACTAATGCAAATGATATAACTCAAAGTCTCACGGGAAAA
                                                                                                                                                                                       AsnAlaSerAlaGluIleLysSerLeuAspGluLysGlnValTyrLeuGluGlnGluIle
                                                                                                                                                                                                                                                                                                                                                                                   MetAlaGlnTrpAspAspPheProAspGlnGlnGluAspThrAspSerCygThrGluSer
                               Aricagecacrescretricaeaarcaacacacacrescrearacrecrearer
                                                                                                             PheValValLeuValProllelleGlylleValAlaAlaGlnLeuLeuLysTrpGluThr
                                                                                                                                             LysAsnCysThrValGlySerValAsnAla---AspIleSerProSerProGluGlyLys
                                                                                                                                                                             GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn
                                                                                                                                                                                                                                                     TTCCAAAATTTCAGCATGACAACTGATCAAAGATTTAATGACATTTCTCTGCAGCTAAGT
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US-10-995-561-370
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                                                                                                                                                                                              PheValValLeuValProlleIleGlyIleValAlaAlaGlnLeuLeuLysTrpGluThr
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|GBAAATGACAGCRAAGAGGAAATGAGATTTCAAGAAGYCTTTATGGAACACATGAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PheglnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCCAAAATTTCAGCATGACAACTGATCAAAGATTTAATGACATTCTCTGCAGCTAAGT
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                        2.82e-101
1016.50
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sapiens
                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                              Alignment Scores:
Pred. No.:
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Tue

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US-10-995-561-371
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Best Local Similarity:
Query Match:
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Pred. No.:
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Sequence 369, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERBNCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeQ for Windows Version 4.0
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                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
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Sequence 371, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 87702

SEQ ID NO 371

LENGTH: 3719 119 259 939 P 234 294 354 414 474 534 MetGluSerArg11eGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139 654 40 9 80 20 9 TMCCTTCAAGAGAARCTGAAGTCCTTCAAAGCTGCACTGRTTGCCCTTTACCTCCTCGTG TTTGCAGTTCTCATCCCTCTCATTGGAATAGTGGCCAGCTCAACTCCTGAAGTGGGAAACG 21 VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro PheValValLeuValProllelleGlyIleValAlaAlaGlnLeuLeuLysTrpGluThr 81 LysAsnCysThrValGlySerValAsnAla---AsplieSerProSerProGluGlyLys GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn 240 LysGlyGluMetLysLeuLeuAsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGlu 1 MetalaGinTrpAspAspPheProAspGinGluAspThrAspSerCysThrGluSer 41 ThrieuGlnGluArgMetLysSerTyrLysThrAlaLeuIleThrLeuTyrLeuIleVal

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LOCATION: (1) ... (119036)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-995-561-13314
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Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERBNCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PASCEGO for Windows Version 4.0
SEQ ID NO 13144
119
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                                                                                                                                                                                                                                                                                                                                                                                          37 LysAsnGlyProThrLeuGlnGluArgMetLysSerTyrLysThrAlaLeuIleThr---
GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn
                MetGluSerArgileGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn
                                                                            160 SerbeubeuserSerlleGlnGluHisGluAsnIleIleGlyAspIleSerbysSerbeu
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ORGANISM: Homo sapiens
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Best Local Similarity:
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LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo E
US-10-995-561-10011
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                              ; ORGANISM: HOMO
US-10-995-561-9974
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLEO POLYMORPHISMS ASSOCIATED WITH
TITLEO POLYMORPHISMS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 9974
                                                                              LeulysTrpGluThrLysAsnCysThrValGlySerValAsnAla---AspIleSerPro
                                                                                                                                                  52113 CGGAATGGAATGATATGGGATGGGATCCTGTATGCATTCAAGGATCASGCCATGACTGGT
                         LeuTyrLeuIleValPheValValLeuValProIleIleGlyIleValAlaAlaGlnLeu
                                                     --- ACAGCTCAACTC
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Sequence 9974, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
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Publication No. US20050272054A1
GENERAL INFORMATION: US20050272054A1
TITLE OF INVENTION: CENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CENETIC POLYMORPHISMS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: ReatSEQ for Windows Version 4.0
SEQ ID NO 10011
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US-10-995-561-10109
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                                                                                                                       APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10046

LENGTH: 201
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| Publication No. US20050272054A1
| GENERAL INFORMATION: USCOMMATION: GENERAL INFORMATION: GENERAL INFORMATION: CARGILL, Michele et al.
| TITLE OF INVENTION: GENERAL DESCRIBERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: CARGILOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
| TITLE OF INVENTION: DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/10/995,561
| CURRENT PILING DATE: 2004-11-24
| NUMBER OF SEQ ID NOS: 85702
| SOFTWARE: FREESEQ for Windows Version 4.0
| SEQ ID NO 10086
| LENGTH: 201
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Matches:
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-995-561-10086
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Best Local Similarity:
Query Match:
DB:
                                                                     10-995-561-10046
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US-10-995-561-10086
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Sequence 10109, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICATION
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOPTHARE: FastSEQ for Windows Version 4.0
LENGTH: 201
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28.10-995-561-9940
; Sequence 9940, Application US/10995561
; Publication No. US20050272054A1
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RESULT 15
US-10-995-561-10049
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APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9940
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FactSEQ for Windows Version 4.0
LENGTH: 201
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; ORGANISM: Homo sapiens
US-10-995-561-9977
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; ORGANISM: Homo sapiens
US-10-995-561-9940
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10014
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Publication No. US200S027205441

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: CARDICOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REPERENCE: CL01559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24
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TITLE OF INVENTION: SCAVENGER RECEPTOR PROTEIN AND ANTIBODY
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US-08-931-399-15

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/307,400
FILING DATE: 16-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 391,486
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: 272,002
FILING DATE: 15-NOV-1988
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SCAVENGER RECEPTOR PROTEIN
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,400
FILING DATE: 16-5EP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 997,113
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 391,486
FILING DATE: 09-AUG-1989
APPLICATION NUMBER: 272,002
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APPLICANT: KREIGER,
TITLE OF INVENTION:
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                               GTGAAGTTCGATGCTCGCTCAGTGACAGCTTTGCTTCCTCCCCATCCTAAAAATGGCCCA
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                                                                                                             187 TCCCTTCAAGAGAAAACTGAAGTCCTTCAAAAGCTGCACTGATTGCCCTTTACCTCCTCGTG
                                                                                                                                                                                                                                                         247 TTTGCAGTTCTCATCCCTCTCATTGGAATAGTGGCAGCTCAACTCCTGAAGTGGGAAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGGAGAAGTGAAAGTACTGAATAACATCACTAATGATCTCAGACTGAAAGATTGGGAA
                                                                                         21 VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro
                                                                                                                                                             41 ThrieuGlnGluArgMetLysSerTyrLysThrAlaLeuIleThrLeuTyrLeuIleVal
                                                                                                                                                                                                                                   PheValValLeuValProllelleGlyIleValAlaAlaGlnLeuLeuLysTrpGluThr
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                       Met AlaGinTrpAspAspPheProAspGinGluAspThrAspSerCysThrGluSer
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ADDRESSEE: SmithKline Beecham - Corporate Patents
ADDRESSEE: U.S.
STREET: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
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Patent No. 5683903
GENERAL INFORMATION:
APPLICANT: Lysko, Paul G.
APPLICANT: Elshourbagy, Nabil A.
APPLICANT: Brawner, Mary B.
TILLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
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US-08-453-117-3
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                                                                                                                   GInGluAsnAlaPheLysGlnGlnGluGluMetArgLysLeuGluGluArglleTyrAsn
                                                                                                                                             756 GGGGAAATGAAACTGTTGAATAATATCACTAATGATGCTGGAGGTTGGGAATTGGAACT
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GlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArgVal
                                                                                       GGTCTGAACACACACAGTACTTGCAGTTCAGTATTGAAACACTGAATGGCAGAGTC
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED.

ITILE OF INVENTION: WITH HUMAN DISEABE, METHODS OF DETECTION AND USES FILE REFERENCE: CLOOJI307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEC ID NOS: 207012

SOFTWARE: FESSEER FOR WINDOWS VERSION 4.0

SEQ ID NO 3387
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Matches:
Conservative:
Mismatches:
Indels:
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1042.50
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72.2%
50.6%
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Best Local Similarity:
Query Match:
DB:
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US-09-949-016-3387
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US-09-949-016-3387
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240 LysGlyGluMetLysLeuLeuAsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGlu 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                            260 HisSerGlnThrLeuLysAsnIleThrLeuLeuGlnGly 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lysko, Paul G.
APPLICANT: Elshourbagy, Nabil A.
APPLICANT: Brawner, Mary E.
TITLE OF INVENTON: Attachment Enhanced 293 Cells
UNDBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,222
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ATTORNEY/AGENT INFORMATION:
NAME: Jervie, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION:
RHOR APPLICATION DATA:
APPLICATION NUMBER: US/08/453,117
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TOPOLOGY: No. 5863798 Relevant
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TELEFAX: (610) 270-5019
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1367 base pairs
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STRANDEDNESS: doub
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| AAGAATTGCTCAGTTAGTTCAACTAATGCAAATGATATAACTCAAAGTCTCACGGGAAAA 366
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COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                      CULANDER DATE:
FILING DATE:
FILING DATE:
FILING DATE:
CLASSIPICATION: 435
ATTORNEY/ABGRT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
FELECOMMUNICATION INFORMATION:
TELEFAX: (610) 270-5019
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1367 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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APPLICATION NUMBER: US/08/453,117
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1042.50
87.2%
72.2%
50.6%
    COUNTRY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
Query Match:
DB:
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LOCATION:
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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7.96e-114
1042.50
87.2%
72.2%
50.6%
                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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187 TCCCTTCAAGAGAAACTGAAGTCCTTCAAAGCTGCACTGATTGCCCTTTACCTCCTCGTG 246
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        MetGluSerArg1leGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139

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TITLE OF INVENTION: Attachment Enhanced 293 Cella NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ANITHKINE Beecham - Corporate Patents U.S. STREET: Mailcode - UW2220, 709 Swedeland Road CITY: King of Prussia STATE: Pennsylvania STATE: Pennsylvania COUNTY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
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197
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,145
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth J. Hecht
REGISTRATION NUMBER: P-41, 824
REFERENCE/COKET NUMBER: P-50338
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: (610) 270-5099
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Conservative:
Mismatches:
Indels:
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1042.50
87.2%
72.2%
50.6%
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TYPE: nucleic acid
STRANDEDNESS: double
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not relevant
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US-08-973-145-3
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Sequence 3, Application US/08973145
Patent No. 5919636
GENERAL INFORMATION:
APPLICANT: Lysko, Paul G.
APPLICANT: Elshourbagy, Nabil A.
APPLICANT: Brawner, Mary E.

US-08-973-145-3

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RESULT 8
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ATGGAGAAAGAGAATCCAGCATATTTTAGACATGGAAGCCAACCTCATGGACACAGAGCAT 486
                     PheGlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn 159
                                                                                     ValGlnGluAsnAlaPheLysGlnGlnGluGluMetArglysLeuGluGluArglleTyr
                                                                                                                                                                                                                    AsnAlaSerAlaGluIleLysSerLeuAspGluLysGlnValTyrLeuGluGlnGluIle
                                     APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: JATA PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                  HisSerGlnThrLeuLysAsnileThrLeuLeuGlnGly 272
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Patent No. 6500938
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1260:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                               Conservative:
Mismatches:
                                                                                                            Length:
Matches:
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                                                                                  7.96e-114
1042.50
87.2%
72.2%
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                               ; CLONE: g219991
US-09-016-434-1260
IMMEDIATE SOURCE:
                                                                                                                                                 Percent Similarity:
                                                                                          Alignment Scores:
                   LIBRARY:
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220 AsnAlaSerAlaGluIleLysSerLeuAspGluLysGlnValTyrLeuGluGluIle 239
                                                                                                        140 PheGlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn 159
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                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lysko, Paul G.
APPLICANT: Elshourbagy, Mabil A.
APPLICANT: Brawner, Mary B.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham - Corporate Patents
ADDRESSEE: U.S.
STREET: Mailcode - UW2220, 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 HisSerGlnThrLeuLysAsnileThrLeuLeuGlnGly 272
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jervis, Herbert H.
REGISTATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/08453117; Patent No. 5683903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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             GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF SEQUENCES:
AUDRESSES: SmithKline Beecham - Corporate Patents U.S.
ADDRESSES: SmithKline Beecham - Corporate Patents U.S.
STREET: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STREET: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STREET: Walloofe - UW2220, 709 Swedeland Road
CITY: U.S.A.
ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sequence 3, Application PC/TUS9608081
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P503:
TELECOWMUNICATION INFORMATION:
TELEFRAN: (610) 270-5019
TELEFAX: (610) 270-5019
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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1042.50
87.2%
72.2%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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PCT-US96-08081-3
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Best Local Similarity:
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        MetAlaGlnTrpAspAspPheProAspGlnGlnGlnGluAspThrAspSerCysThrGluSer

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Mismatches:
Indels:
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                                                                 Length:
Matches:
                                                               1.5e-113
1042.50
87.2%
72.2%
50.6%
                            47..1402
                                                                                           Best Local Similarity:
Query Match:
MOLECULE TYPE:
FEATURE:
NAME/KEY: CDS
LOCATION: 47.
                                                                                 Percent Similarity
                                                      Alignment Scores:
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RESULT 10

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197
41
34
1
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,222
FILING DATE:
FLING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              Patents
                                       GENERAL INFORMATION:
APPLICANT: Lysko, Paul G.
APPLICANT: Bishourbagy, Nabil A.
APPLICANT: Bishourbagy, Nair B.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSE:
ADDRESSEE: GaithKline Beecham - Corporate Patent
ADDRESSEE: U.S.
                                                                                                                                                                                                               STREET: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: U.S.A.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: SBC-P50338
TELECOMUNICATION INFORMATION:
TELEPHONE: (610) 270-5090
INFORMATION FOR SEQ IN NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2028 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: No. 5863798 Relevant
; Sequence 1, Application US/08948222
; Patent No. 5863798
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NAME/KEY:
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                                           GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn 119
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                                                                                         MetGluSerArgileGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139
                                                                                                                                   PheGlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn 159
                                                                                                                                                                               SerLeuLeuSerSerlleGlnGluHisGluAsnIleIleGlyAspileSerLysSerLeu 179
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| AAGAATTGCTCAGTTAGTTCAACTAATGCAAATGATATAACTCCAAAGTCTCACGGGAAAA
                                                                                                       AsnAlaSerAlaGlulleLysSerLeuAspGluLysGlnValTyrLeuGluGlnGlulle
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LysAsnCysThrValGlySerValAsnAla --- AspIleSerProSerProGluGlyLys
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                                                                                                                                                                                                                                                                                                                                                                                                                 HisSerGlnThrLeuLysAsnileThrLeuLeuGlnGly 272
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lysko, Paul G.
APPLICANT: Blshourbagy, Nabil A.
APPLICANT: Brawner, Mary E.
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-5090
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SmithKline Beecham - Corporate Pate STREET: Mailcode - UW2220, 709 Swedeland Road CITY: King of Prussia CITY: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/973,145
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
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NAME: Elizabeth J. Hecht
REGISTRATION NUMBER: P-41, 824
REFERENCE/DOCKET NUMBER: P50338
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08973145
Patent No. 5919636
GENERAL INFORMATION:
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GlyAanGlySerGluAapGluMetArgPheArgGluAlaValMetGluArgMetSerAsn 119
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                           CDNA to mRNA
                                                                                                                                                                                                                                                                                  1.5e-113
1042.50
87.2%
72.2%
50.6%
TELEFAX: (610) 270-5090 INPORMATION POR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 2028 base pairs
                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA to mi
FEATURE:
                                                                                                                        not relevant
                                                                                                                                                                                                      47..1402
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Best Local Similarity:
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80

346

406

166

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466

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179

586 199 646

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120 MetGluSerArgIleGlnTyrLeuSerAspAsnGluAlaAsnLeuLeuAspAlaLysAsn 139
                                                                                        GlyAsnGlySerGluAspGluMetArgPheArgGluAlaValMetGluArgMetSerAsn
                                                                                                                                                                                          ValGlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArg
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                                                                                                             140 PheglnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn
                                                                                                                                                                                                                                                                  467 TTCCAAAATTTCAGCATGACAACTGATCAAAGATTTAAATGACATTCTTCTGCAGCTAAGT
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               LyskanCysThrValGlySerValAsnAla---AspIleSerProSerProGluGlyLys
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COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk

COMPUTER: IBM PC compatible

COMPUTER: PC COMPATION

SOFTWARE: PEADELT INFORMATION:

RATIORNEY/AGENT INFORMATION:

NAME: PADEL PATION NUMBER: 31,284

REGISTRATION NUMBER: 31,284

REGISTRATION NUMBER: MIT6392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08154365; Patent No. 5624904; GENERAL INFORMATION: APPLICANT: Besnick, David APPLICANT: Resnick, David APPLICANT: Kreiger, Monty APPLICANT: Kreiger, Monty APPLICANT: Joiner, Keith APPLICANT: Joiner, Keith APPLICANT: Joiner, Keith APPLICANT: JOINER OF INVENTION: Septicemia NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: 3 ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Atlanta
STATE: Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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767 AAAGGAGAAGTGAAAGTACTGAATAACATCACTAATGATCTCAGACTGAAAGATTGGGAA 826
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                                                                                                                                     Sequence 1, Application PC/TUS9608081
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Attachment Enhanced 293 Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham - Corporate Patents U.S.
STREET: Mailcode - UW2220, 709 Swedeland Road
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: U.S.A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08081
                                                        827 CATTCTCAGACCTTGAGAAATATCACTTTAATTCAAGGT
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: P503
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (610) 270-5019
TELEFAX: (610) 270-5019
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2028 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: CDNA to mRNA
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Query Match:
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587 ATAAGTTTGAATACCACATTGCTTGATTTGCAGCTCAACATAGAAAATCTGAATGGCAAA 646
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Patent No. 576739
GENERAL INFORMATION:
APPLICANT: BASZCZYNSKI, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.29e-72
688.00
98.5%
97.7%
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 484 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 PheGlnAsnPheSerIleThrThrAspGlnArgPheAsnAspValLeuPheGlnLeuAsn 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 SerieuLeuSerSerIleGlnGluHisGluAsnIleIleGlyAspIleSerLysSerLeu 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 ValGlyLeuAsnThrThrValLeuAspLeuGlnPheSerIleGluThrLeuAsnGlyArg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 VallysPheAspAlaArgSerValThrAlaLeuLeuProProHisProLysAsnGlyPro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrieuGlnGluArgMetLysSerTyrLysThrAlaLeuIleThrLeuTyrLeuIleVal 60
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196
42
34
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Matches:
Conservative:
Mismatches:
Indels:
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TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6508
TELEFAX: (404)-815-6508
TELEFAX: (404)-815-6508
TEROTATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                   RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             3.44e-113
1039.50
87.2%
71.8%
50.5%
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PUBLICATION INFORMATION:
AUTHORS: Ashkenas, et al.
JOURNAL: J. Lipid Res.
                                                                                                                                                                                  ORGANISM: homo sapien
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                      PAGES: 983-1000
DATE: 1993
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                 240 LysGlyGluMetLysLeuLeuAsnAsnIleThrAsnAspLeuArgLeuLysAspTrpGlu 259
                                                                                                                                                                                                                                                                                 767 AAAGGAGAAGTAAAGTACTGAATAACATCACTAATGATCTGAGACTGAAAGATGGGAA 826
                                   200 ValGinGluAsnAlaPheLysGlnGlnGluGluMetArgLysLeuGluGluArglleTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BASZCZYNSKI, Chris
APPLICANT: HOOD, Elizabeth
APPLICANT: MADDOCK, Sheila
APPLICANT: MEYER, Terry Euclaire
APPLICANT: REGISTER III, James C.
APPLICANT: WITCHER, Derrick
APPLICANT: HOWARD, John A.
TITLE OF INVENTION: PLANTS
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: MEANINGLESS D.C.
COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: TBM PC compatible
COMPUTER: US/08/54.506
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/54,586
FILING DATE: 06-NOV-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: BRAT'S tephen A:
REGISTRATION NUMBER: 29,768
RESTRENCE/POCKET UNMBER: 33229/352/PIHI
TELEPPONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                        260 HisserGinThrLeuLysAsnileThrLeuLeuGinGly 272
                                                                                                                                                                                                                                                                                                                                                                                                         827 CATTCTCAGACCTTGAGAAATATCACTTTAATTCAAGGT 865
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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STRANDEDNESS:
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US-08-831-399-3
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; Sequence 3, Application US/08831399
; Patent No. 6312916
; GENERAL INFORMATION:
    APPLICANT: Kopetzki, Erhard; Muller, Rainer;
    APPLICANT: Ropetzki, Erhard; Muller, Urban; Deger, Arno; Brandstetter, Hans
    TITLE OF INVENTION: Recombinant Inactive Core
    TITLE OF INVENTION: Recombinant Inactive Core
    TITLE OF INVENTION: Streptavidin Mutants
    NUMBER OF SEQUENCES: 16
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Pelfe & Lynch
    STARE: New York
    CONTRY: USA
    STARE: New York
    COUNTRY: USA
    ZIP: 10022
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
    COMPUTER: IBM PS/2
    COMPUTER: IBM PS/2
    COMPUTER: 18M PS/2
    COMPUTER: 18M PS/2
    COMPUTER: 18M PS/2
    COMPUTER: 18M DATA:
    SOFTWARE: Watcherfeet
    CURRENT APPLICATION NUMBER: US/08/831,399
    FILLIG DATE: 1-April-1997
    CORRESPONDENCE
                                                                                                                            SerAsnMetThrIleGlyAlaValAsnSerArgGlyGluPheThrGlyThrTyrIleThr 307
                                                                                                                                                                                                                AlavalThrAlaThrSerAsnGluIleLysGluSerProLeuHisGlyThrGlnAsnThr 327
                                                                                                                                                                                                                                           GCCGTGACCGCCACCTCCAACGAGATCAAGGAGTCCCCCTCCACGGTACCCAGAACACC 248
                                                                                                                                                                                                                                                                                                  IleAsnLysArgThrGlnProThrPheGlyPheThrValAsnTrpLysPheSerGluSer 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGTGGCTCCTGAGGAGCTCCGTGAATGACATCGGCGACGACTGGAAGGCCACCGCGCGTG 428
                                                                                                                                                                                                                                                                                                                                               ATCAACAAGAGGACCCAGCCCACCTTCGGCTTCACCGTGAACTTGGAAGTTCTCCGAGTCC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCACCGTGTTCACCGGCCAGTGCTTCATCGACCGCAACGGCAAGGAGGTGCTCAAGACC 368
                                       268 ThrieuLeuGlnGlyAlaArgLysCysSerLeuThrGlyLysTrpThrAsnAspLeuGly
                                                                                                                                                      TCCAACATGACCATCGGCGCGTGAACTCCAGGGGCGAGTTCACCGGCACCTACATCACC
                                                                  69 TCCCTCGCCAGCGCGCCAGGAAGTGCTCCCTCACCGGCAAGTGGACCAATGACCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlylleAsnilePheThrArgLeuArgThrGlnLysGlu 400
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US-10-618-570-2 (1-400) x US-08-554-586-1 (1-484)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PREPLICATION NUMBER: 10 5 37 718.8
FILING DATE: 16-September-1996
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 6312916man D. REGISTRATION NUMBER: 30,946
REPERENCE/DOCKET NUMBER: 4105
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 604 base pairs
TYPE: nucleic acid
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US-08-831-399-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerSerValAsnAspIleGlyAspAspTrpLysAlaThrArgValGlyIleAsnIlePhe 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerAsnGluIleLysGluSerProLeuHisGlyThrGlnAsnThrIleAsnLysArgThr 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 GGCCAGTGCTTCATAGACAGGAATGGGAAGGAGGTCCTGAAGACCATGTGGCTGCTGCGG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 rcaagigiraargacarregreargacregaaagcraccagggregecarcaacarcrrc 475
                                                                                                                                                                                                                                                                                                                                                                                                                        116 GCCAGAAAGTGCTCGCTGACTGGGAAATGGACCAACGATCTGGGCTCCAACATGACCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 TCAAATGAGATCAAAGAGTCACCACTGCATGGGACACAAAAACACCATCAACAAGAGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 GlyAlaValAsnSerArgGlyGluPheThrGlyThrTyrIleThrAlaValThrAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 GGGCTGTGAACAGCAGAGGTGAATTCACAGGCACCTACATCACAGGCGCGTAACAGCCGAA
                                                                                                                                                                                                                                                                                                                                                                                               273 AlaArglysCysSerLeuThrGlyLysTrpThrAsnAspLeuGlySerAsnMetThrIle
                                                                                       Positions 44..115 correspond to sig
peptide and 116..499 to mat peptide
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0 0 0
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Matches:
Conservative:
Mismatches:
Indels:
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Job time : 239 secs
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                                                                                                                                                                                           5.07e-71
678.00
100.0%
100.0%
32.9%
TOPOLOGY: linear FEATURE:
NAME/KEY: CDS
LOCATION: 44..499
OTHER INFORMATION: P
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Best Local Similarity:
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During Linear Control of Control 
AR102094 Sequence
AF132211 Cloning v
AR164477 Sequence
D88622 Bicistronic
158322 Sequence 6
158323 Sequence 6
160509 Sequence 6
160509 Sequence 6
177052 Sequence 6
187735 Sequence 6
187735 Sequence 6
187735 Sequence 6
187743 Sequence 6
187743 Sequence 6
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AB041928 Retrovira
AB041928 Retrovira
AB08518 Setrovira
AR321727 Sequence
AR321725 Sequence
AR55176 Sequence
AR55175 Sequence
AR55175 Sequence
BD075836 Retroviru
BD081937 Method. 8
BD26912 Retroviru
AR59118 Sequence
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A61K37/02
Strandedness: Single;
Topology: Linear;
Biotin-binding receptor molecule
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5177; Conservative 0; Mismatches
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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4200 3720 3480 4020 4080 4260 GTGCACCTCCAAGCTTCACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTAAAGGAAG 3601 GCTGGGGGCCCTCTGGTAAGGTTGGAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTG 3661 CCGCCAAGGATCTGATGGCGCAGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCG TTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGG CTATTCGGCTATGACTGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGG CATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTG GACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGTCAAGGCGCGCATG GACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCGTG cccaccaccaccarcicercarcccarcccarccarccracricerraccaaararcarccra ATTGTATTTTAAGTGCCTAGCTCGATACAGCAAACGCCATTTGACCATTTCACCACATTGGT GTGCACCTCCAAGCTTCACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAG CGGAACACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCAGCTAC CTTACATGGCGATAGCTAGACTGGGCGCTTTTATGGACAGCGAACCGGAATTGCCA CCGCCAAGGATCTGATGGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCG CTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGG GAACTGCAGGACGAGGCAGCGCGTATCGTGGCTGGCCACGACGGCGTTCCTTGCGCA GAACTGCAGGACGAGGCAGCGATACGTGGCTGGCCACGACGGCGTTCCTTGCGCA GCTGTGCTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCCGAAGTGCCG GCTGTGCTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCG CATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTG

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TRLRTQKE"
YLA HERTTUALA SEPPO (FI); AIRENNE KARI (FI); KULOMAA MARKKU (FI);
MARJOMAKI VARPU (FI); LEHTOLAINEN PAULIINA (FI); EUROGENE LIMITED
(GB)
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Benkel, B.F. and Falconer, M.M.
TRANS-SOMATICS WITH GENE TRANSFER INTO MAMMARY EPITHELIAL CELLS
PATENT: WO 9943795-A 1 02-SEP-1999;
BENKEL BENHARD F (CA); FALCONER MARCIA M (CA)
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Query Match 40.2%; Score 2078.8; DB 6; Length 7699; Best Local Similarity 64.3%; Pred. No. 0; D Matches 3339; Conservative 0; Mismatches 1814; Indels 38; Das 14; Qy 1 TTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCAAGGCAT 234 D D Conservation of Caractaactaactaactaactaactaactaactaactaac		TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCTGTACCTTATTTGAC TAACCAATCAGTTCGCTTCTGGTTCGCGCGCTTCCGCTCTCCGAGCTCAATAAA TAACCAATCAGTTCGCTTCTGGTTCGCGCGCTTCCGCTCTCCGAGCTCAATAAA TAACCAATCAGTTCGCTTCTGGTTCGCGCGCTTCCGCTCTCCGAGCTCAATAAA AAAGCCCAATCAGTTCGCTTCTGTTCGCGCTTCCGCTCTCCGAGCTCAATAAA AAAACCCAATCAGTTCGCTTCTGTTCGCGTTCTGTTCGCGTTCTGCGCTCAATAAA AAAACCCAAACCCTCAACCCGCGCGCATCTCCGATAACTGCGTCGCCCCGCCCG	655 CCGTATTCCCAATAAAGCCTCTTGCTGTTTTGCAATCGTGGTCTCGCTGTTCCTTG 657 CCGTATTCCCAATAAAGCCTCTTGCTGTTTTGCAATCGTGGTCTCGCTGTTCCTTG 715 GGAGGGTCTCCTCTGAGTGATTGACTACCCACGAGGGGTCTTTCATTTGGGGGCTCGT 601 CCGGGATTTGGAGACCCCTGCCAGGGACCACCACGGGGGGTCTTTCATTTGGGGGCTCGT 775 CCGGGATTTGGAGACCCCTGCCAGGGACCACCACGGGAGGTAAGCTGGCC 661 AGCAACTTATGGAGACCCCTGCCCAGGGACCACCGGGGAGGTAAGCTGGCC 661 AGCAACTTATGGAGACCCTGCCCAGGACCACCGGGGAGGTAAGCTGGCC 661 AGCAACTTATGGAGACCCAGGACCACCGGGGAGGTAAGCTGGCC 661 AGCAACTTATGGAGACCACCGAGGACCACCGGGGAGGTAAGCTGCG 661 AGCAACTTATGGAGACCACCAGGACCACCGGGGAGGTAAGCTGCG 661 AGCAACTTATGGAGACCACCAGGACCACCGGGAGGTAAGCTGCG 661 AGCAACTTATGGAGACCACCAGGAGCACCACCGGGGAGGTAAGCTGCG 661 AGCAACTTATGGAGACCACCAGGACCACCGGGAGGTAAGCTGCG 661 AGCAACTTATGGAGACCACCAGGAACCACCGGGAGGTAAGCTGCG 661 AGCAACTTATGGAGACCACCAGGAGACCACCGGGAGGTAAGCTGCG 661 AGCAACTTATGGAGACCACCAGGAGACCACCGGGAGGTAAGCTGCG 661 AGCAACTTATGGAGACCACCAGGAGACCACCAGGAGAGCACCACCGGGAGGA	DB 835 AGCAACTTATCTGTGTCTGTTCTGTGTGTTTTGTTTTGT
Db 4591 GCGAATGGCCTGCTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCA 4650	467 AGAGGTTCGGATGAGGAACGGATGGAACGGATGAGGAGGATGATGAGGGCCAACGGATGATGAGGATGATGAGGATGATGAGGATGATGAGGATGAT	4847 GCTCCCAAGGCCTCCCCCTCAGCAGTTTCTAGGGAACCATCAGATTTCCAGGGT 490 5011 GTCCCCAAGGCCTCCAGCAGTTTCTAGGGAACCATCAGATGTTTCCAGGGT 507 4907 GCCCCAAGGACCTGAAATGCCCTGTGCCTTATTTGAACTAACCAATCAGTTTCCAGGGT 507 5071 GCCCCAAGGACCTGAAATGCCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTC 496	5027 GGGGCCCAGTCCCCATTGACTCGCCCGGTACCCGTGTATCCATAAACCCTC 5191 GGGGCGCCAGTCCCGATTGACTGGTCCCCGGTACCCGTGTATCCAATAAACCCTC 5191 GGGGCGCCAGTCCCCGATTGACTGGTCCCCGGGTACCCGTGTATCCAATAAACCCTC 5087 TTGCAGTTGCATCCGACTTGTGGTCTCCTTGCGAGGGTCCCTCTGAGTGATT 5251 TTGCAGTTGCATCCGACTTGTGGTCTCCTTGGGAGGGTCTCCTTGGGAGGTTTCATTTGG 5117 GACTACCCGTCAGGGGGTCTTTCATTTGG 5311 GACTACCCGTCAGGGGGTCTTTCATTTGG 5311	RESULT 5 AR381629 LOCUS AR381629 AR381629 AR381629 ACCESSION AR381629 VERSION AR381629 Unknown. Unclassified. Unclassified. Unclassified. Inchases 1 to 7699) AUTHORS AUTHOR

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TITLE Enhancement of neuron generation and survival JOURNAL Patent: WO 2004062554-A 6 29-JUL-2004; NSGENE A/S (DK) Location/Qualifiers 1. 7436 organism="synthetic construct" Mol_type="unassigned DNA" db_xref="taxon:32630" note="viral vector"	Query Match 38.1%; Score 1972.6; DB 6; Length 7436; Best Local Similarity 65.1%; Pred. No. 0; 0; Mismatches 1529; Indels 281; Gaps 20; Matches 3371; Conservative 0; Mismatches 1529; Indels 281; Gaps 20; 1 TTTGAARGACCCCACCCGTAGGTGGCAAGCTTAAGTTAACGAAGGCAT 60 Introduced Conservation of the c	GGAAAAATACATAACTGAGAATAGAAAGTTCAGATCAAGGTCAGGAACAAGAAACAGC 	121 TGAGTACCAAACAGGATATCTGTGGTAAGCGGTTCCTGCCCCGGCTCAGGGCCAAGAACA 180 181 GATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGG 240 181 GATGAGACAGCTGAGTGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGTGCCCCGG 240	241 CTCGGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA 300 [11	TAACCAATCAGTTCGCTTCTGCTTCTGTTCGCGCGCTTCCGGTCTCCGAGCTCAATAA	421 AGAGCCCACACACCCTCGGCGCCGCCAGTCTTCCGATAGACTGCCCGGGGTAC 480 481 CCGTATTCCCAATAAAGCCTCTTGCTTTGCATCCGAATCGTGGTCTCGTGTTCCTTG 540 481 CCGTATTCCCAATAAAGCCTCTTGCTGTTTGCAATCGTGGTCTTCGTGTTTTCTTG 540 481 CCGTATTCCCAATAAAGCCTCTTGCTGTTTGCAATCGAATCGTGGTCTTCGTTG 540	gaagggretectetgagtgattgaetaeceacgaeggggggggggerggggggggggggggggggg	601 CCGGGATTTGGAGACCCCTGCCCAGGGACCACCACCACCACCGGGAGGTAAGCTGGCC 660	TCTGTACTAGTTAGCTAACTCGTATCTGGCGGACCCGTGGTAGTTAGCGCGGGCTTTCTGTAGTTAGCTAACTCGTGGTGTTTTTGGTGGAACTGGAGTTTTTTGTAGTTAGCTTAGCTCGTGGTGCGGGGCCCGTGGTGGGGGAACTGACGAGGTTTAGCTAACTCGTGTTTTTGGCGGACCCGTGGTGGAACTGACGAGGTT	781 CTGAACACCCGGCCGCAACCCTGGGAGACGTCCCAGGGACTTTGGGGGCCCTTTTTGTGG 840 [1][1][1][1][1][1][1][1][1][1][1][1][1][

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BD138566.1 GI:22233511

BD138566.1 GI:22233511

3 JP 2002508976-A/5.

8 synthetic construct
synthetic construct
other sequences, artificial sequences.

1 (bases 1 to 7546)

2 Radosevich, T.J. and Jr.C.J.L.

Expression system of nucleotide with reduced immunogenicity for use in gene therapy
In gene therapy
Patent: JP 2002508976-A 5 26-MAR-2002;
HUMAN GENE THERAPY RESEARCH INSTITUTE
OS Artificial Sequence
PN JP 2002508976-A/5

PD 26-MAR-2002
                  DNA linear PAT 18-SEP-2002
with reduced immunogenicity for use
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F 14-JAN-1998 US 60/071409
I THOMAS J RADOSEVICH, CHARLES J LINK JR
C12N15/09, A61K31/711, A61K48/00, A61P37/06, C12N1/15, C12N1/19,
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Description of Arrificial Sequence : recombinant vector FH Location/Qualifiers

source 1. .7546

/organism='Arrificial Sequence'.
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_kref="taxon:32630"
                  BD138566 7546 bp Expression system of nucleotide
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                                                                                                     CATGCCCGACGGCGAGGATCTCGTCGTCACCCATGGCCGATGCCTTGCCGAATATCAT 4316
                                                                                                                    CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGC 4436
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1661 GATCCGGCTGTGGAATGTGTCAGTTGAAACACTCCCAGGCAGG	1774 ¢CCCAGGCTCC¢ÁGCAÁGCÁGAAÁTÁTGCAÁAGCATÓCATCTCAÁTTÁGTCÁGCÁACCA 1833 1741 AAATTAAGTCTCTAGATGAAAACAAGTATATTGGAACAGGAAATAAAAGGGGAAATGA 1800 1741 AAATTAAGTCTCTAGATGAAAAACAAGTATATTTGGAACAGGAAATAAAAGGCGCCCATTC 1891 1801 AACTGTTGAATAATAATCACTAATGATCTGAGGCTGAAGGATTGGGAACATTCTCAGACAT 1860 1801 AACTGTTGAATAATAATAATGATCTGAGGCTGAAGGATTGGGAACATTCTCAGACAT 1860 1892 TCCGCCCCATGGCTGAATAATTTTTTTTTATGCAAAGGCCGCCTCGGCCTC 1951	1861 1952 1921 1994 1981	2054 CCGCGTCGACGGATGAACCTTGTAATGCTTAGTCTGAGCCCTCTGGGCCCCGGTCGCGGGT 2113 2041 CACAAAACACCATCAACAAGAGGACCCAGCCCACTTTGGCTTCACCGTCGAAGT 2100 2114 AGTATGCCTGAATTATCCTTGACTCTTTCGATGAACTCGCCCTTGGTG 2164 2101 TTTCAGAGTCCACTGTCTTCACGGCCAGTGCTTCATAGAAGAATGGGAATGGGAAGGAGG 2160 2165 GAGACGGAGCGGTTGTCTTCACGGCCAGTGCTTCATAGACAGGAATGCGAATGCGAAGGAGG 2160 2165 GAGACGGAGCGGTTGTCTTCACGGAGTATTCGGAAGTACCGGAGTACCGAAGAATTCCGAAGTATTCCGAAGTATTCCGAAGTATTCCGAAGTATTCCGAAGTATTCCGAAGTAATTCCAAGTAATTCCAAGTAATTCCAAGTAATTCCAAGAATTCCAAGAATTCCAAGAATTCAAGTAATTCCAAGAATTCAAGAATTCAAGAATTCAAGAATTCAAGAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAGAAATTCAAAAAAAA	2161 TCCTGAAGACCATGGGGTGCTGAAGTGTTAATGACATTGGTGATGACGGAAAG 2225 GCGCCTGCGTGCTCCGATCGGCGCTCGACTGGAGGCTCTGTGGACCCTGCGCGGGAAC 2221 CTACCAGGGTGCATCAACATCTTCACTCGCCTGCGCACAGAAGGAGGAGTGAGT	2281 ACCAAGGTCCTCCTGGACTCCAGGTGAAAAGGAGATAGAGGCCCTCCTGGACAAATGG 2340	2451 TTTCCCCTGCCACCAAACTTATTATGTAGGTGCGAACCCCGGTGCTGGGCTCGTGC 2459 ACTTAATGGACAAAAAAGGCAGAAAAAAAAGGAGAGAGGAAGCAAAAAA	2571 GTCTAATGGCGTACTACGCGCTCACGATTAAGTCGGCGCAGTATACGCTGATGA 2624 2579 CGAAGGCCAGTGGGTACGGTGTGACGCCGCTGGAACTGCGTGGAGGACTGCTGTGTGTG
540 714 600 774 660			10.75	1163		CGGTTGGCTCAGTTAATGCAGATATCTCCAAGTCCGGAAGGCAAAGGAATGGCAGTG 1380	1441 TCCAGTATCTTTCAGATAATGAAGCCAATCTCCTAGATGCTAAGAATTTCA 1500 1541 CCTCCTCTTCTCCTCCTCCTCTTTTCCTTTCAAGATTTCA 1500 1551 CCTCCTTTCTTCCTCCCCTTGAAGATTTTAATGATGTTTTTCTTTTCCAGCTAAATTTCCT 1500 1501 GCATAACAACTGATCAAAGATTTAATGATGTTCTTTTCTTTTCCAGCTAAATTCCTTACTTTCCT 1560 1601 CGATCCTCCCTTTATCCAGCCCTCACTCCTTCTTTAGGAGAATTCGTTAACTAGAAGA 1660 OX 1561 CCATCCAGGAACATGAGAATATCATAGGAGAATTCTCCAAGTCTTAAGTAGGTCTGAACA 1620 OX

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235 GGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCAGGAACAAGAACAGC 294 121 TGAATACCAAACAGGATATCTGGGTAAGCGGTTCCTGCCCGGGTCAGGGCCAAGAACA 180 295 TGAATACCAAACAGGATATCTGTGGTAAGCGGTTCCTGCCCGGGTCAGGGCCAAGAACA 354 181 GATGAGACAGCTGAATACTGTGGTAAGCGGTTCCTGCCCGGGTCAGGGCCAAGAACA 354 182 GATGAGACAGGTGATGGGCCAAACAGGGATATCTGTGGTAAGCAGTTCCTGCCCCGG 240 355 GATGAGACAGGTGATGGTCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGG 414 241 CTCGGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA 300 415 CTCGGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCCAGCCCTCAGCAGTTTCTAGTGAA 474 301 CCATCAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA 474	475		AGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTGATGTTTATGCGCCTGCG		1021 TCANTTCGGCACGAGTAANTCGGTGCTGCCGTCTTTAGGACATATGAAGTATGCCACAGT 1080 1163
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Qy 4819 TGCCCCGGCTCAGGGCCAAGAACAGATGCTCCCCAGTCCTCAGCAGTTT 4878 Db 4830 TGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCTCAGCAGTTT 4889 Qy 4879 CTAGAGAACATCAGATGTTTCCAGGGTGCCCCAAGAACCCTGTGCCTTA 4938 Db 4890 CTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGAACCTGTGCCTTA 4949 Qy 4939 TTTGAACTAACCAATCAGTTCGCTTCTGGTTCGGTGCTTCTGCTCCCCGAGCT 4998 Qy 4930 TTTGAACTAACCAATCGTTCGCTTCTGTTCGGCGCTTCTGCTCCCCGAGCT 5009 Qy 4950 TTTGAACTAACCAATCGTTCGCTTCTGTTCGGCGCTTCTGGTCCCCCGAGCT 5009 Qy 4950 CAATAAAAGAGCCCACAACCCCACACCCACCCAACTCCGGGCTTCTGATTCAGCTGCCCGAGCT 5009 Qy 4950 CAATAAAAAGAGCCCACAACCCCACACCCACCCAGGCCCAGCTCCCGATTGACTGAGTGGCC 5058 Db 5010 CAATAAAAAGAGCCCACAACCCCTACTCGGGGGCCCAGTCCTCCGATTGACTGAGTGGCC 5069	Qy 5059 CGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTGGTGT 5118 bb 5070 CGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCACTTGTGGTCTGGTGT 5129 Qy 5119 TCCTTGGGAGGGTCTCCTGAGTGATTGACTACCGTCAGCGGGGGTCTTTCATTTGG 5177 Db 5130 TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGGTCTTTCATTTGG 5188	RESULT 8 BD138564 LOCUS LOCUS LOCUS DEFINITION Expression system of nucleotide with reduced immunogenicity for use in gene therapy. ACCESSION BD138564 VERSION BD138564.1 GI:23233509 KERYMORGS JP 2002508976-A/3. SOURCE Synthetic construct ORGANISM Synthetic construct ORGANISM Synthetic construct Corber sequences; attificial sequences. REPERRORE (Dases 1 to 7165)	A C 4 D N N O F S H D	ES	Ouery Match Query Match Query Match Best Local Similarity 62.9%; Pred. No. 0; Matches 3284; Conservative 0; Mismatches 1309; Indels 624; Gaps 23; Qy 1 TTGAAAGACCCCACCCGTAGGTGGCAAGCTAAGTAACGCCACTTTGCAAGGCAT 60 Db 175 TTTGAAAGACCCCACCGTAGGTGGCAAGCTAAGTAAGTAA

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3358 GGTGTGCACCTCCAAGCTTCACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAA 3415 	3416 GGAAGCGGAACACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCA 3475 	3476 GCTACTGGGCTATCTGGACAAQGGAAAACGCAAGCGCAAAGAGAAAGCAGGTAGCTTGCA 3535 	3536 GTGGGCTTACATGGCGATAGCTAGACTGGGGGGTTTTATGGACAGCGAACCGGAAT 3595	3596 TGCCAGCTGGGGCCCCTCTGGTAAGGTTGGGAAGCCCTGCAAAGTAAACTGGATGGCTT 3655	3656 TCTTGCCGCCAAGGATCTGATGGCGCAGGGGATCAGATCTGATCAAGAGACAGGATGAG 3715 1	3716 GATCGTTTCGCATGATTGAACAAGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGG 3775	3776 AGAGGCTATTCGGCTATGGCCACAACAGACAATCGGCTGCTGTGATGCCGCCGTGT 3835	3836 TCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACC	3896 TGAATGAACTGCAGGACGAGGAGCGCGCTATCGTGGCCACGACGGCGTTCCTT 3955	3956 GCGCAGCTGTCCTCGACGTTGTCACTGAAGCGGAAGGGACTGGCTGCTATTGGGCGAAG 4015	4016 TGCCGGGGAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGG 4075	4076 CTGATGCAATGCGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACAGG 4135	4136 CGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATG 4195	4196 ATCTGGACGAAGAGCATCAGGGGCTCGCCCGAACTGTTCGCCAGGCTCAAGGCGC 4255-	4256 GCATGCCCGACGGCGAGGATCTCGTCGTCGACCCATGGCGATGCCTGCTTGCCGAATATCA 4315	4316 TGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGTGTGGCGGACC 4375	4376 GCTATCAGGACATAGGGTTGGCTACCGGGATATTGCTGAAGAGCTTGGCGGCGAATGGG 4435	4436 CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCT 4495
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2281 ACCAAGGTCCTCCTGGACTCCAGGTGAAAAAGGAGTAAGAGGCCCTCCTGGACAAAATGG 2340	2341 TATACCAGGCTTTCCAGGTCTAATAGGTACTCCAGGTCTTAAAGGTGATCGGGGGGATCT 2400	CTGGTTTACCTGGAGTTCGAGGATTCCCAGGACCAATGGGGAAGACCGGGAAGCCAGGAC 246	TTAATGGACAAAAAGGCCAGAAGGGAGAAAAAGGGAGTGGAAGCATGCAAAGACATCTA 252		GTCGTCT	2641 GCAGGAGCTTGGGATACAAAGGTGTTCAAAGTGTGCGTAAGCGAGCTTATTTTGGAAAAG 2700 	GTACGGGTCCAATATGCCTGAATGAAGTATTTTGTTTCGGGAAAGAGTCATCCATTGAAG	2172 2761 AGTGCAGAATTAGACAGTGGGGTGTGAGAGCCTGTTCGCACGACGAAGATGCTGGGGGTC 2820 2172 2172	ACTITIGCACCTACATAATGCATCATATTTTCATTCACCATTTTTAAACTGTTATAAAGTG 	GCTTCACTAAAATCAGCTTAATTAATATTTAAGAAACTAAGAATTTT		GCTICAAATACCAGAACCATTICAACTICTCTAGGITTITAAGTG 	CTTATGC CTTATGC	AAGGAGA AAGGAGA	32	33	CCACATT 335	2520 AMITGIMITTAMGTGCCIMGCICGMIACAGCAMAGGCCATTITTGACCATTCACCACATT 25/9

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2761 AGTGCAGAATTAGACAGTGGGGTGTGAGAGCCTGTTCGCACGACGAAGATGCTGGGGTC 2820 2172	2941 ATCCACAGAAAAGGAATATTTAAAAATCACTGGATAAACATATAAAATAGCTTCATATTT 3000 2208ACCGACAACTTT 2219 3001 GCTTCAAATACCAGAAACACTTCTAGGTTTTTAAGTGGCTGGTGCGAATTG 3060	3061 ATCCCTCAGGATATAGTAGTTTCGCTTTTGCATAGGAGAGAAATGTAGTCTTATGC 3120	3181 GAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTCGTGCCTTATTAGG 3240 [3301 -ATTGTATTTAAGTGCCTAGCTCGATACAGCAAACGCCATTTGACCATTCACCACATT 3357	GGAAGCGGAACACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCA 	2700 GCTACTGGGCTATCTGGACAAGGGAAGCGCAAGGCGCAAGGCAAGGCAGGTAGCTTGCA 2759 3536 GTGGGCTTACATGGCGATAGCTAGACGGGGTTTTATGGACAGGAAGGGAACGGAAT 3595 2760 GTGGGCTTACATGGCGATAGCTGGGCGGTTTTATGGACAGCAAGCGAACGGAAT 2819 3596 TGCAGCTGGGAGCCCTGGTAAGGTTGGGAAGGTAAGTAAACTGGGAAT 3655	2820 TGCCAGGGGGGGCCCTCTGGTTGGTTGGGAAGCCTTGTAAACTGGTTGGT	3716 GATCGTTTCGCATGATTGAACAAGATGCATTGCACGCGGGTTCTCCGGCCGCTTGGGTGG 3775 2940 GATCGTTTCGCATGATTGAACAAGATGCACGTTTCCCGGCCGCTTGGGTGG 2999 3776 AGAGCTATTCGGCTATGACTGGCCACAACAGCAATCGGCTGCTCTGTGCGCCGCTTGGGTGG 2999 3700 AGAGCTATTCGGCTATGACTGGCCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGT 3835 3000 AGAGCTATTCGGCTATGACTGGGCCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGT 3059 3836 TCCGGCTGTCAGCGCAGGGCCCCGGTTCTTTTGTCAAGACCGATGCCGGTGCT 3059
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TAAACAACAAGAGAGAGATGGGTAAATTAGAGGAGCGTATATACAATGCATCAGCAGGAGGTATATATA	1725 ANC	1981 CCTACATCACAGCCGTAACAGCCACATCAAATGAGATCAAAGAGTCACCACTGCATGGGA 2040 1982TACTTACGCAAGAACATTGTACTAAAAATGCATGCATGGCA 1829 2041 CACAAAACTGCCATCAACAAGAGCCAGCCCACCTTTGGCTTCACGTCAATTGGAAGT 2100 1830AAAACTGCCTGTAAAATAGACCTATTGAAAAGTATTGTGGACTTGTGGGT 1884	AAGGAGG TTTATAT TGGAAAG	TCTTCACTCGCCTGCGCACACAGAAGGAGTGAGTGAGTG	2006 AACAATATCTGAACCTTTACCCGGTGGCGGCA	2040		AGGACCTATTTTGGAAAG

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TITGAMAGACCCCACCCGTAGGTGGCAAGCTTAAGTAACGCCACTITGCAAGGCAT TITGAAAGACCCCACCCGTAGGTGGCAAGCTTAAGTAACGCCACTITGCAAGGCAT GGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAGGTCAGGACAAAAGAAACAGC GGAAAAATACCTAACTGAGAATAGAAAAGTTCAGATCAGGTCAGGACAACAGC TGAATACCAAACAGGATTTCTGGTAACTGGTAACTGCCCCGGCTCAGGGCCAAGAACA GATGAACAGACAGAATATCTGTGGTAACTGGTTCTTGCTCGCCCCGGCTCAGGGCCAAGAACAG TGAATACCAAACAGGATATCTGTGGTAACTGGTTCTTGTGCTCCCCCGGCTCAGGGCCAAGAACAG GATGAACAGCTGAGTGATGTAACTGTGAACACAGGATTCTTGTGTAATACCAAACAGAACAGAACACAGAACAGAACAGAACAGAACAGAACAGGATTCTGTGTACCTGTCTGT	CCGGGCGCAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGR CCGGGCGCAACCTGGGAGACGTCCAGGGACTTTGGGGGCCGTTI CCCGGCCGCAACCCTGGGAGACGTCCAGGGACTTTGGGGGCCGTTI CCCGGCCGCAACCCTGGGAGACTCCAGGACTTTGGGGGCCGTTI CCCGGCCGCAACCTGGGAGTTGGAGTTTTGGTGGTTGGTGGGGGGCCGTTI CCCGGCGTCTGGAGTTGGAGTTGGGGTGGGGCGGTGGGGGGGCGTTGGGGGGGG
6868686868686868686	8 8 8 8 8 8 8 8 8
90 80 11 61 10 70 70 11 18 11 4 78 18 18 18 18 18 18 18 18 18 18 18 18 18	DEFINITION Sequence 9 from Patent W00202738. ACCESSION AX302149.1 GI:19576958 KEYWORDS SOURCE SOURCE SOURCE SOURCE SOURCE OFFICE STATE CONSTRUCT OCHARICA OFFICE STATE SEQUENCES. REFERENCE OFFICE STATE SEQUENCES. REFERENCE OFFICE SEQUENCES. AUTHORS Bremel, R.D., Miller, L.U., Bleck, G.T. and York, D. TITLE Host cells containing multiple integrating vectors JOURNAL Patent: W0 0202738-A 9 10-JAN-2002; FEATURES JOURNAL Gala Design, Inc. (US) FEATURES SOURCE ADDITIONAL LYPOR—"Unassigned DNA" ADD_XTEF="taxon:32630" ORIGIN QUERY MATCH Guery MATCH GALE SIMIlarity 66.1%; Pred. NO. 0; Matches 3007; Conservative 0; Mismatches 754; Indels 786; Gaps 18;

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	2341 TATACCAGGCTTTCCAGGTCTAATAGGTACTCCAGGTCTTAAAGGTGATCGGGGGGATCT 2040	Oy 2461 TTAATGGACAAAAGGCCAGAAGGGAGAAAAAGGCATGGAAAGCATCTA 2520 Db 2040	Db 2108 GCCGCATGCGGGACCTTGTGGCTCCTCTGCCG	2761 AGTGCAGAATTAGACAGTGGGGTGTGAGAGCCTGTTCGCACGAAGATGCTGGGGGTC 2172	Qy 2881 ATTTTTTCCTTTGCTTCATAAATCAGCTTAATTAATATAAGAAACTAAGAATTTT 2940 Db 2208	Db 2220 GTGTCCTCTCGGAATACCTCTTTCTTGCTTGGGTGTGTGT
1081 GGGATGACTTTCCTGATCAGCAAGACACTGACAGAGTCTGTACAGAGTCG 1140 1060 AGGACCCTGCTCGTTACAGGCGGGGTTTTTCTTGTTGACAAGATCCTCAATACC 1119 1141 ATGCTCGCTCAGTGATACAGGCGGGGTTTTCTTGTTGACAAGAATCCTCAATACC 1119 1120 AGGAGTCTAGAAGCTTTGCTTCCTCCCCCATCTTAGGGCCCAACTCTTCAAG 1200 1120 AGAGATGAAGCTCTATAAAAACTGCACTGATCACCCTTAATCTCATTGTGTTC 1260	1180 TGGCCAAATTCGCAGTCCCCAACCTCCAATCACCTCTTGTCCTCCAATTTG 1239 1261 TGGTGCCCATCATTGGCATAGTGGCAGCTCCTGAAATGGGAAACGAACATTTG 1320			1550 -ČTČÁĞTTTACTÁĞTĞĞTTĞTTCÁĞTĞGTÇTÇĞTÁĞĞĞCTTTCCÇCCÁCTĞTTĞ 1605 1681 CATTTAAACAACAAGAGAGATGCGTAATTAGAGGAGCGTATATACAATGCATCAGCAG 1740 1606 GCTTTCAGTTATATG-GATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCTTGAGTC 1606 1741 AAATTAAGTCTCTAGATGAAAACAAGTATTTGGAACAGGAAATAAAAGGGGAAATGA 1800 1741 AAATTAAGTCTCTAGATGAAAAACAAGTATTTTGGAACAGGAAATAAAAGGGGAAATGA 1800 1665 CCTTTTTACCTCTATATCCTATTTTCTTTTGTAGGTATACATTTAAACCCTAATAA 1724		1782

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1656. 2450

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QDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
2467^2468
                                                                                                                                                                                                                                                                                                                                                                                                                        Miller, A.D.

Miller, A.D.

Direct Submission

Submitted (12-SEP-1989) A.D. Miller, Program in Molecular Medicine,
Fred Hutchinson Cancer Research Center, Seattle, WA 98104, USA

4 (bases 1 to 5464)

Miller, A.D. and Rosman, G.J.

Improved retroviral vectors for gene transfer and expression

BioTechniques 7 (9), 980-982 (1989)
                                                                                                                                                                                                                                                                            SYN 05-JAN-2001
                                       3600 GCTATCAGGACATAGCGTTGCTACCCGTGATATTGCTGAAGAGCTTGCGGCGAATGGG
                                                                                                     CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCT
                   GCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTTGGCGGCGAATGGG
                                                                                     CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCT

    5464
    forganism="Retroviral vector plN"
    fmol type="genomic DNA"
    db xref="taxon:147131"
    noce="derived from Moloney murine leukemia virus"
    144^145

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                                                                                                                                                     vector
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1616^1617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Mo-MuLV DNA end-plasmid pBR322 DNA
                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="mouse DNA end, Mo-MuSV DNA start"
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/note="Mo-MuLV 3' long terminal repeat"
                                                                                                                                                                                                                                                                                                                                             genome, neomycin phosphotransferase, retroviral
Retroviral vector pLN
Retroviral vector pLN
                                                                                                                                                                                                                                                                                                                                                                                             other sequences, artificial sequences, vectors 3 (bases 1 to 5464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Tn5 DNA end, MoMuLV DNA start"
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/note="extended packaging signal" 1133'1134
                                                                                                                                                                                                                                                                   5464 bp DNA Retroviral vector pLN, complete sequence. M28245
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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Best Local Similarity
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                                                                                                                      3660
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DEFINITION
ACCESSION
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                                   -ATTGTATTTAAGTGCCTAGCTCGATACAGCAAACGCCA--TTTGACCATTCACCACATT
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S Whitheric construct
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SM syntheric construct
Other sequences; artificial sequences.

SE I (bases I to 5874)
S Radosevich T.J. and Jr.C.J.L.
Expression system of nucleotide with reduced immunogenicity for use in gene therapy
AL Expression system of nucleotide with reduced immunogenicity for use therapy RESEARCH INSTITUTE
S Artificial Sequence
N AT FIGURAL SOURCE SOU
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Description of Artificial Sequence : recombinant vector FH Location/Qualifiers
source 1. 5874
                                                        2693 AACAGAIGGAACAGCIGAAIAIGGGCCAAACAGGAIAICIGIGGIAAGCAGIICCCGCCC
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2993 ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTT
                                                                                                                                                                      CGGCTCAGGGCCAAGAACAGATGCTCCCCAGATGCGGTCCAGGCCCTCAGCAGTTTCTAGA
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xrefe"taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1486; Conservative 0; Mismatches
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